

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2003, 15:22:35 ; Search time 2415 seconds
(without alignments)
5205.968 Million cell updates/sec

Title: SEQ14-JOIN-SEQ4
Perfect score: 2250
Sequence: 1 NPVLYVDYSCYLPPLPPHRLVS.....PVKIDSDSGKSETRVQNGRS 432

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2244	99.7	1521	6	AX358169 Sequence
2	2243	99.7	1521	6	AX358177 Sequence
3	2240	99.6	1521	6	AX358171 Sequence
4	2237	99.4	1521	6	AX358163 Sequence
5	2234	99.3	1521	6	AX358167 Sequence
6	2233	99.2	1521	6	AX358175 Sequence
7	2198.5	97.7	1518	6	AX358165 Sequence
8	2198.5	97.7	1524	6	AX358159 Sequence
9	2198.5	97.7	1525	6	AF009563 Brassica
10	2191.5	97.4	1518	6	AX358173 Sequence
11	2191.5	97.4	1524	6	AX358189 Sequence
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13	2191.5	97.4	1588	6	AX083739 Sequence
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34	2015	89.6	1521	6	AX473308 Sequence
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ALIGNMENTS

RESULT 1

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LOCUS AX358169 1521 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 13 from Patent WO0194565.
ACCESSION AX358169
VERSION AX358169.1 GI:18674878
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaworski, J.G. and Blacklock, B.J.
TITLE Fatty acid elongase 3-ketocacyl coa synthase polypeptides
JOURNAL Patent: WO 0194565-A 13 13-DEC-2001,
MIAMI UNIVERSITY (US)
FEATURES
source
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Location/Qualifiers
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/note="5', 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
3', 1179 bp from B. napus elongase KCS (SEQ ID NO:3),
having a mutation at position 275; designated At114 K92R"
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BASE COUNT 412 a 342 c 344 g 423 t
ORIGIN

Alignment Scores:
Pred. No.: 1,03e-197 Length: 1521
Score: 2244.00 Matches: 431
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 1
Query Match: 99.73% Indels: 0
DB: 6 Gaps: 0

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Qy 41 GlyThrCysAspAspSerSerTrpLeuaspPheLeuArgLysIleGlnLuarqSerGly 60
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Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGCGGATGAACTCACGGGCGGAGGGCTGCTTCAGGTCCCTCCCGCGGAAGACTTTT 462

Qy 81 AlbalAlaArgGluCluThrGluGlnValIleleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 CGCGCGCGCGGTGAAGACGAGGACGAGATTATCATTTGGTGGCTCAGAAATCTATTCAAG 522

Qy 101 AsnThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsn 120
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Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
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Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
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Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
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Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
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Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSer 280
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RESULT 2
LOCUS AX358177 1521 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 21 from Patent WO0194565.
ACCESSION AX358177
VERSION AX358177.1 GI:18674886
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM

artificial sequences.

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REFERENCE
AUTHORS      Jaworski, J.G. and Blacklock, B.J.
TITLE        Fatty acid elongase 3-ketocacyl coa synthase polypeptides
JOURNAL      Patent: WO 0194565-A 21 13-DEC-2001;
             MIAMI UNIVERSITY (US)
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DEFINITION Sequence 15 from Patent WO0194565.
ACCESSION  AX358171
VERSION     AX358171.1  GI:18674880
KEYWORDS   'synthetic construct.
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SOURCE      '
ORGANISM   '
REFERENCE   1
AUTHORS     Jaworski, J.G. and Blacklock, B.J.
TITLE       Fatty acid elongase 3-ketocacyl coa synthase polypeptides
JOURNAL     Patent: WO 0194565-A 15 13-DEC-2001;
            MIAMI UNIVERSITY (US)
FEATURES    Location/Qualifiers
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source

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CDS

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QY 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
Db 1363 GGGTCAGGCTTTAAGTGTACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAGCTTCG 1422
QY 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAATAGTCTCTGGGAACACTGCATCGACAGATACCCGCTCAAAATTTGATTTCTGATTC 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAAGTCAGAGACTGCTGTCCAAAACGGTCGGTCC 1518
RESULT 4
AX358163 1521 bp DNA linear PAT 13-FEB-2002
LOCUS Sequence 7 from Patent WO0194565.
DEFINITION AX358163
ACCESSION AX358163
VERSION AX358163.1 GI:18674872
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaworski,J.G. and Blacklock,B.J.
TITLE Fatty acid elongase 3-ketoacyl coA synthase polypeptides
JOURNAL Patent: WO 0194565-A 7 13-DEC-2001;
MIAMI UNIVERSITY (US)
FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="5' 342 bp from A. thaliana FAEL (SEQ ID NO:1) and
3' 1179 bp from B. napus elongase KCS (SEQ ID NO:3);
designated At114"
1. .1521
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CDS

Alignment Scores:

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Pred. No.: 2,41e-197 Length: 1521
Score: 2240.00 Matches: 430
Percent Similarity: 99.77% Conservative: 1
Best Local Similarity: 99.54% Mismatches: 1
Query Match: 99.56% Indels: 0
DB: 6 Gaps: 0
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SEQ14-JOIN-SEQ4 (1-432) x AX358171 (1-1521)

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QY 21 ValSerLysValMetAspPheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db 283 GTCTCTAAAGTCATGGATATTTCTAGCAATTAAGAAAGCTGATCTTCTACGGAAC 342
QY 41 GlyThrCysAspAspSerSerTrpLeuAspPheArgLysIleGlnGluArgSerGly 60
Db 343 GGACAGTGTGATGATCTGCTGGCTTGACTTCTTGAGGAAGATTCAAGAAGCTTCAGGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGGCGATGAACACTCAGGCGCGAGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTT 462
QY 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCGCGCGCGGTGAGAGACGCGACAGTATCATTTGGTGGCTGAGAAATCATTTCAAG 522
QY 101 AsnThrAsnValAsnProLysAspIleGlyLysLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAACGTTTAAACCTTAAAGATATAGGTATATCTTGTGGTGAACATCAAGCATGTTAAT 582
QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCATCGCTCTCCGCGATGGTGTTCACCTTTCAAGCTCCGAGCAGCATGTAAGA 642
QY 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAAACCTTGGTGGGATGGGTGTGAGTGGCGGCTTATAGCCATTGATCTAGCAAG 702
QY 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTTCATGCTCCATAAAATACGATAGCTCTTGTGGTGAGCAGACAGACATCACT 762
QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
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GGMGCSAGVIAIDLAKDLHVKNTYALVYSTENITNYAGDNRSMMVSNCLFRVGG
AAILLNKGEDRRRSKVELVHTHTGADGKFRVCQGDDENGKIGVSLSKDITDV
AGTRVKNKLTGPIPLPLSEKLLFFVTFMGKKLFKDKIKHYVPDFKLAIDHPCIH
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BASE COUNT 413 a 342 c 342 g 423 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 4,56e-197 Length: 1521
Score: 2237.00 Matches: 429
Percent Similarity: 99.54% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.42% Indels: 0
DB: 6 Gaps: 0

SEQ14-JOIN-SEQ4 (1-432) x AX358163 (1-1521)

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Db 223 AATCCGGTTTATCTCGTTGACTACTCGTTACCTTCCGCCACCGCATCTCAAAGTTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
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Db 283 GTCCTAAAGTCATGGATATTTCTACCAATAAGAAAGCTGATCTCTTCACGGAAC 342
Qy 41 GlyThrCysAspAspSerSerTyrLeuAspPheLeuArgLysIleGlnIleArgSerGly 60
|||||
Db 343 GGCACGCTGTGATGATTCGTCGTGCTTGACTTCTTGAGGAAGATTCAAGAAGCTTCAGGT 402
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
|||||
Db 403 CTAGGCGATGAACATCACGGGCCCGAGGGCTGCTTCAGGTCCCTCCCGCAAGACTTTT 462
Qy 81 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
|||||
Db 463 GCGGCGCGCGTGAAGAGACGGAGCAAGTTATCATTTGGTGGCTAGAAAAATCTATTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
|||||
Db 523 AACACCAACCTTAAACCTTAAGATATAGGTATGATCTTGGTGAACCTCAAGCATGTTTAA 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
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Db 583 CCAACTCCATCTCTCCGCGATGGTGGTAAACACTTTTCAAGCTCCGAAGCAACGTAAGA 642
Qy 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
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Db 643 AGCTTAACTTGGTGGCATGGGTGTGTGGCGGCTTATAGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
|||||
Db 703 GACTTGTTCATGCTCCATAAAATACGTATGCTTGTGGTGAGCAGACAGAACATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
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Db 763 TATAACATTTACGCTGGTGGTAAATAGTCCATGATGTTTCAAAATGCTTGTTCCTGGT 822
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
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Db 823 GGTGGGCGCGCTATTTGCTCTCCAACAGCCCTGGAGATCGTAGACGGTCCCAAGTACGAG 882
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
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Db 883 CTAGTTTCACAGGTTTCGACACGCATACCGAGCTGACGGCAAGTCTTTTCGTTGGCTGCAA 942
Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
|||||
Db 943 CAAGGAGACGATGAGAACGGCAAAATCGAGTGGATTTGTCCAAGGACATACCGATGTT 1002
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
|||||
Db 1003 GCTGGTCCGAAAGGTTAAGAAAAACATAGCAACGTTGGGTCGTTGATTCTTCCGTTAAGC 1062
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
|||||
Db 1063 GAGAAACTCTTTTTTTCGTTTACCTTCATGGCAAGAAACTTTTCAAGATATAAATCAA 1122
Qy 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
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Db 1123 CATTACTACGTCCTCCGGATTCAAACTTGCTATTGACCATTTTGTATACATCGCGGAGGC 1182
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
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Db 1183 AGAGCCGTGATTGATGCTAGAGAAGAACCTAGCCCTAGCACCGATCGATGAGAGCA 1242
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Db 1243 TCAAGATCAACGTTTACATAGATTGGAACACTTCATCTAGCTCAATATGGTATGAGTTG 1302
Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
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Db 1303 GCATACATAGAACAAAGAGGATGAAGAAGGTATAAAGTTTGGCAGATTGCTTTA 1362
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer 400
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Db 1363 GGGTCAGGCTTTAAGTGTACAGTCAGTTTGGGTGGCTCTAAACATGTCAAGCTCG 1422
Qy 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
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Db 1423 ACAAAATAGTCTTTGGGAACACTGCATCGACAGATACCGGTCAAAATTCATTCTGATTCA 1482
Qy 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
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Db 1483 GGTAACTCAGAGACTCGTCCCAACACGTCGGTCC 1518
RESULT 5
AX358167 1521 bp DNA linear PAT 13-FEB-2002
LOCUS Sequence 11 from Patent WO0194565.
DEFINITION AX358167
ACCESSION AX358167
VERSION AX358167.1 GI:18674876
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaworski,J.G. and Blacklock,B.J.
TITLE Fatty acid elongase 3-ketoacyl coa synthase polypeptides
JOURNAL Patent: WO 0194565-A 11 13-DEC-2001;
MIAMI UNIVERSITY (US)
FEATURES Location/Qualifiers
source
1. .1521
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="5' 342 bp from A. thaliana FAEL (SEQ ID NO:1) and
3' 1179 bp from B. napus elongase KCS (SEQ ID NO:3) having
mutations at positions 271, 272 and 275; designated At114
L91C K92R"
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CDS

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BASE COUNT 413 a 341 c 344 g 423 t

ORIGIN

Alignment Scores:

Pred. No.: 8,63e-197 Length: 1521
Score: 2334.00 Matches: 429
Percent Similarity: 99.54% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.29% Indels: 0
DB: 6 Gaps: 0

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QY	21	ValSerLysValMetAspIlePheTyrClnIleArgLysAlaAspThrSerSerArgAsn	40
DB	283	GTCTCTAAAGTCATGGATATTTCTACCAATAAGAAAGCTGATACCTCTTCACGGAAC	342
QY	41	GlyThrCysAspSerSerTrpLeuAspPheLeuArgLysIleGlnLysArgSerGly	60
DB	343	GGCAGCTGTGATAATTCGTGCGGTGACTCTCTCAGGAAGATTCAGAACGTTACAGT	402
QY	61	LeuGlyAspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPhe	80
DB	403	CTAGGCGATGAAACTCACGGCCGAGGGGCTGCTTCAGGTCCCTCCCGGAGACTTTT	462
QY	81	AlaAlaAlaArgGluCluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys	100
DB	463	CGCGCGCGCGGTGAGAGACGAGCAAGTATCATTTGGTGGCTAGAAAATCTATTCAAG	522
QY	101	AsnThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsn	120
DB	523	AACACCAACTTAACCCTAAGATATAGGTATACTTGTGTGCAACTCAAGCATGTTTAA	582
QY	121	ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg	140
DB	583	CCAACTCCATCGCTCTCCCGATGGTGGTAACTTTCAAGCTCCGAGCAAGCAAGTAAGA	642
QY	141	SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys	160
DB	643	AGCTTTAACTTGGTGGCATGGTGTAGTCCGCGGCTTATAGCCATGTATGACCAAG	702
QY	161	AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr	180
DB	703	GACTTGTTCATGTCCATAAAATACGTATGCTTGTGGTGAGCAGACAGAAATCATCT	762
QY	181	TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal	200
DB	763	TATAACATTTAGCTGGTGGTAAATAGGTCCATGATGTTTCAATGCTTCTTCGCGGTT	822
QY	201	GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu	220
DB	823	GGTGGCGCGCTATTTTCTCTCCCAACACCTCGGAGATCGTGTACGCTCCAGTAGAG	882
QY	221	LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln	240
DB	883	CTAGTTTCACACGGTTCGAACGCATACCGGAGCTTGACGGCAAGCTTTTCGTTGCGTCAA	942
QY	241	GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal	260
DB	943	CAAGGAGACGATGAGAACCGCAAAATCGGAGTGAGTTGTCCAGGACATACCGATGTT	1002
QY	261	AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer	280

DB	1003	CTGGTGGCAACGGTTTAAAGAAAACATAGCAACGTTGGGTCCGTTGATTCTCTCGTTAAAC	1062
QY	281	GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys	300
DB	1063	GAGAAATCTCTTTTTCGTTACCTTCATCATGGGCAAGAAATTTTCAAAGATAAATCAAA	1122
QY	301	HisTyrTyrValProAspPheLysLeuAlaIleAspPheLysPheCysIleHisAlaGlyGly	320
DB	1123	CATTACTAGTCCCGGATTTCAAACTTGCTATGTACCATTTTGTATACATGCGGAGGC	1182
QY	321	ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla	340
DB	1183	AGAGCGGTGATTGATGCTAGAGAAGAACCTAGCCCTAGCACCGCATCGATGAGGCA	1242
QY	341	SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrGluLeu	360
DB	1243	TCAAGTCAACGTTACATAGATTTGGAAACACTTCATCTAGCTCAATATGATGATGTTG	1302
QY	361	AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTyrGlnIleAlaLeu	380
DB	1303	GCATACATAGAAGCAAAAGGAAGGATGAAGAAGTAATAAAGTTTGGCAGATTGCTTTA	1362
QY	381	GlySerGlyPheLysCysAsnSerAlaValTyrValAlaLeuAsnAsnValLysAlaSer	400
DB	1363	GGGTGAGCTTTAAGTGTAACTGACGTGCGTTCGGTGGCTCTAAACAATGTCAAAGCTCG	1422
QY	401	ThrAsnSerProTyrGluHisCysIleAspArgTyrProValLysIleAspSerAspSer	420
DB	1423	ACAAATAGTCTCTGGGAACACTGCATCGACAGATACCCGGTCAAAATGATTGATCTGATCA	1482
QY	421	GlyLysSerGluThrArgValGlnAsnGlyArgSer	432
DB	1483	GGTAACTCAGAGACTGTCGCCAAACGTCGCTCC	1518

RESULT 6

AX358175 LOCUS AX358175 1521 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 19 from Patent WO0194565.
ACCESSION AX358175
VERSION AX358175.1 GI:18674884
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaworski, J.G. and Blacklock, B.J.
TITLE Fatty acid elongase 3-ketoacyl coa synthase polypeptides
JOURNAL Patent: WO 0194565-A 19 13-DEC-2001,
MIAMI UNIVERSITY (US)

FEATURES

source Location/Qualifiers
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/db_xref="taxon:32630"
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1..1521
/note="unnamed protein product"
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/protein_id="CAD23308.1"
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AAILSNSPGRRSKSELVHTHTGADGSKSPRVOQDDENKRGISVLSKLDITDV
AGRTVKKNIAITLGPLLILPSEKLLFFVFMGKKLFKDKIRHYVDPDFKLAIDHFCIHA
GGRAVIDLEKNLALAPIDVEASRSTLHRFGNTSSSIWYELAYIEAKGRMKGNKRVW
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BASE COUNT 415 a 340 c 343 g 423 t
ORIGIN

Alignment Scores:
Pred. No.: 1,07e-196 Length: 1521
Score: 2233.00 Matches: 429
Percent Similarity: 99.54% Conservatively: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.24% Indels: 0
DB: 6 Gaps: 0

SEQ14-JOIN-SEQ4 (1-432) x AX358175 (1-1521)

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QY 21 ValSerLysValMetAspIlePheThrGlnIleArgLysAlaAspThrSerArgAsn 40
Db 283 GTCCTTAAGTCATGGATATTTCTACCAATTAAGAAAGCTGATCTTCTACCGAAC 342
QY 41 GlyThrCysAspSerSerThrLeuAspPheLeuArgLysIleGlnArgSerGly 60
Db 343 GGCACGCTGTAAATTCGTCGCTGACTTCTTGTAGGAAGATTCAAGAACGTTTCAGGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGCGGATGAACATCACGGGCGCGAGGGCTGCTTCAGGTCCTCCCGGAAGACTTTT 462
QY 81 AlaAlaAaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCGGGCGCGCTGAAGACAGCGAGCAAGTTATCATTTGGTGGCTGAGAAATCTATTCAAG 522
QY 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 ACACCAACGTTACCTTAAGATATAGGTATGTTGTTGGTGAACCTCAACCATGTTTAT 582
QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCNACTCGATCGCTCCGGGATGGTTCGTTAACTTTCAAGCTCCGGAACAGTAAAG 642
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Db 643 AGCTTTAACCCTTGGTGGCATGGGTTAGTGGCGCGGTTATAGCCATTGATCTAGCAAG 702
QY 161 AspLeuLeuHisValHisLysAsnThrThrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTTGTTGCATGTCATATAAATAAGTATGCTCTTGGTGGACACAGAAACATCACT 762
QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGGTGATANTAGTCCATGATGGTTTCAATTCGTTCCGTTGT 822
QY 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysThrGlu 220
Db 823 GTGGGGCGCGTATTTGCTCTCAACAAGCCCTGGAGATCTAGACGGTCCAAAGTACGAG 882
QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTACACGGTTCGAACGCATCCGGAGCTGACGACAGTCTTTTCGTCGGTGAA 942
QY 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
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QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGGTCAACCGTTAAGAAACATAGCAACGTTGGTCCGTTGATTCCTCGTTAAGC 1062
QY 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
Db 1063 GAGAAACTCTCTTTTTCGTTACCTTCATGGGCAAGAAACACTTTTCAAGAGATAAAATCAAA 1122

QY 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
Db 1123 CATTACTAGTCCCGGATTTCAAACTTGCTATTGACCATTTTGTATACATGCCGGAGC 1182
QY 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
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QY 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrTyrGluLeu 360
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QY 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValThrPcInIleAlaLeu 380
Db 1303 GCATACATAGAAAGCAAGAGGAGGTAAGAAAGGTAATAAAGTTTGGCAGATTGCTTTA 1362
QY 381 GlySerGlyPheLysCysAsnSerAlaValThrValAlaLeuAsnValLysAlaSer 400
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QY 401 ThrAsnSerProThrGluHisCysLysIleAspArgTyrProValLysLysAspSer 420
Db 1423 ACAATAGTCTTTGGGAACACTGTCATCGACAGATACCCGGTCAAAATTTGATCTGATTC 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAGTACAGACTCGTGTCCAAACGGTGGTCC 1518
RESULT 7
AX358165 1518 bp DNA linear PAT 13-FEB-2002
LOCUS Sequence 9 from Patent W00194565.
DEFINITION AX358165
ACCESSION AX358165
VERSION AX358165.1 GI:18674874
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Jaworski, J.G. and Blacklock, B.J.
TITLE Fatty acid elongase 3-ketoacyl coA synthase polypeptides
JOURNAL Patent: WO 0194565-A 9 13-DEC-2001;
MIAMI UNIVERSITY (US)
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BASE COUNT 415 a 343 c 344 g 416 t
ORIGIN

Alignment Scores:
Pred. No.: 1,64e-193 Length: 1518
Score: 2198.50 Matches: 423
Percent Similarity: 98.84% Conservatively: 3
Best Local Similarity: 98.14% Mismatches: 4

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DB:	6	Gaps:	1
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QY	42	ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu	61
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QY	402	AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly	421
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DEFINITION	Sequence 3 from Patent WO0194565.		
ACCESSION	AX358159		
VERSION	AX358159.1		
KEYWORDS	GI:18674868		
SOURCE	rape.		
ORGANISM	Brassica napus		
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AUTHORS	Jaworski,J.G. and Blacklock,B.J.		
TITLE	Fatty acid elongase 3-ketoacyl coa synthase polypeptides		
JOURNAL	Patent: WO 0194565-A 3 13-DEC-2001;		
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ORIGIN			
Alignment Scores:			
Pred. No.:	1.65e-193	Length:	1524
Score:	2198.50	Matches:	423
Percent Similarity:	98.84%	Conservative:	3
Best Local Similarity:	98.14%	Mismatches:	4
Query Match:	97.71%	Indels:	1
DB:	6	Gaps:	1
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DEFINITION AF009563
ACCESSION AF009563.1 GI:2271464
VERSION AF009563.1
KEYWORDS
SOURCE Brassica napus.
ORGANISM Brassica napus.
REFERENCE 1 (bases 1 to 1525)
AUTHORS Clemens, S. and Kunst, L.
TITLE Isolation of a Brassica napus cDNA (Accession No. AF009563) encoding 3-ketoacyl-CoA synthase, a condensing enzyme involved in the biosynthesis of very long chain fatty acids in seeds (PGR97-125)
JOURNAL Plant Physiol. 115, 313-314 (1997)
REFERENCE 2 (bases 1 to 1525)
AUTHORS Clemens, S. and Kunst, L.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1997) Botany, University of British Columbia, 6270 University Blvd., Vancouver, BC V6T 1Z4, Canada
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BASE COUNT 422 a 350 c 344 g 409 t
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Alignment Scores:
Pred. No.: 1,65e-193 Length: 1525
Score: 2198.50 Matches: 423
Percent Similarity: 98.84% Conservative: 3
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 97.71% Indels: 1
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DEFINITION Sequence 17 from Patent WO0194565.
ACCESSION AX358173
VERSION AX358173.1 GI:18674882
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaworski, J.G. and Blacklock, B.J.
TITLE Fatty acid elongase 3-ketoacyl coa synthase polypeptides
JOURNAL Patent: WO 0194565-A 17 13-DEC-2001;
MIAMI UNIVERSITY (US)
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DB: 6 Gaps: 1

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 DEFINITION Sequence 33 from Patent WO0194565.
 ACCESSION AX358189
 VERSION AX358189.1 GI:18674898
 KEYWORDS synthetic construct.
 SOURCE artificial construct.
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Jaworski, J.G. and Blacklock, B.J.
 TITLE Fatty acid elongase 3-ketoacyl coa synthase polypeptides
 JOURNAL Patent: WO 0194565-A 33 13-DEC-2001;
 MIAMI UNIVERSITY (US)
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 Pred. No.: 7,29e-193 Length: 1524
 Score: 2191.50 Matches: 422
 Percent Similarity: 98.61% Conservative: 3
 Best local Similarity: 97.91% Mismatches: 5
 Query Match: 97.40% Indels: 1
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 Db 289 TCCAAGGTCTAGTATCTTTTATCAAGTAAAGAAAGCTGAT---CCTTCTCGGAACGCC 345
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 Db 346 ACGTCCGATGACTCGTGGCTTGTGACTCTTTGAGAGAGATTCAGAACGTTCAAGTCTA 405
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QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
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Db 1486 AAGTCAGACACTCGTGTCCAAAACGGTCCGCTCC 1518

RESULT 12
AX473307

LOCUS AX473307 1524 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 17 from Patent WO02052024.
ACCESSION AX473307
VERSION AX473307.1 GI:22207959
KEYWORDS
SOURCE rape.
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1

AUTHORS Wilmer, J. A. and Wallington, E. J.
TITLE Elongase promoters
JOURNAL Patent: WO 02052024-A 17 04-JUL-2002;
BIOGEMMA UK LIMITED (GB)
FEATURES Location/Qualifiers
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BASE COUNT 423 a 350 c 342 g 409 t
ORIGIN

Alignment Scores:

Pred. No.: 7,29e-193 Length: 1524
Score: 2191.50 Matches: 422
Percent Similarity: 98.61% Conservative: 3
Best Local Similarity: 97.91% Mismatches: 5
Query Match: 97.40% Indels: 1
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LOCUS AX083739 1588 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 17 from Patent WO0111061.
ACCESSION AX083739
VERSION AX083739.1 GI:13185467
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 1588)
AUTHORS Kunst, L. and Clemens, S.
TITLE Regulation of embryonic transcription in plants
JOURNAL Patent: WO 0111061-A 17 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
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Alignment Scores:
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Query Match: 97.40% Indels: 1
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DEFINITION
ACCESSION AF274750
VERSION AF274750.1 GI:14495234
KEYWORDS
SOURCE Brassica napus.
ORGANISM Brassica napus.
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1. (bases 1 to 1704)
Han, J., Luhs, W., Sonntag, K., Zahringer, U., Borchardt, D. S.,
Wolter, F. P., Heinz, E. and Frentzen, M.
Functional characterization of beta-ketoacyl-CoA synthase genes
from Brassica napus L.
Plant Mol. Biol. 46 (2), 229-239 (2001)
21335051
11442062
2. (bases 1 to 1704)
Han, J., Wolter, F. P. and Frentzen, M.
Direct Submission
Submitted (02-JUN-2000) Institute of General Botany, University of
Hamburg, Ohnhorststr. 18, Hamburg, Hamburg 22609, Germany
Hamburg, Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 8,52e-193 Length: 1704
Score: 2191.50 Matches: 422
Percent Similarity: 98.61% Conservative: 3
Best Local Similarity: 97.91% Mismatches: 5
Query Match: 97.40% Indels: 1
DB: 8 Gaps: 1
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QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
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Db 229 CCGGTTTACCTCGTGTGACTCATCTACCTTCCACCACGCATTGTAGATCAAGATATC 288
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|||||
QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
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Db 346 AGCTCGCATGACTCGCTGGCTTGACTTCTTGAGGAAGATTCAAGAACGTTTCAGGTCTA 405
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QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
|||||
Db 406 GCGCATGAAACTCACGGGCCCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTGGG 465
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QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
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Db 466 GCGGCGCTGGAAGAGCGGAGCANGTTATCATGTGCGCTAGAAAATCTATTCAAGAAC 525
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QY 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
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QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
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Db 586 ACTCCATCGCTCTCCGCGATGCTGCTTAACACTTTCAGCTCCGAAACACGTAAGAACG 645
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QY 142 PheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
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QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
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QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
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Db 766 AACATTTACGCTGCTGATATAGGTCATGATGTTTCAAAATGCTTGTTCGCTGTTGGT 825
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QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
|||||
Db 826 GGGGCGCTATTTTGTCTCCACACAGGCTGGAGATCGTAGCGGTCGCAAGTACGAGCTA 885
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QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
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Db 886 GTTCACACGGTTCGAACGCATACCGGAGCTGACGACACGCTTTTTCGTTGCGTGCACAA 945
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QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
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QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
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QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLysLeuPheLysAspLysIleLysHis 301
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Qy 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
 Db 1507 AATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAAATTGATTCTGATTCAGGT 1566

Qy 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
 Db 1567 AAGTCAGAGACTCGTGTCCAAAACGGTCGGTCC 1599

Search completed: January 6, 2003, 18:09:32
 Job time : 2441 secs

GenCore version 5.1.3
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Run on: January 6, 2003, 16:31:35 ; Search time 39 Seconds
(without alignments)
3397.035 Million cell updates/sec

Title: SEQ14-JOIN-SEQ4

Perfect score: 2250

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2015	89.6	1641	4	US-09-362-633-1
3	1524.5	67.8	1611	4	US-08-868-373-9
4	1508.5	67.0	1548	4	US-08-868-373-13
5	1492.5	66.3	1479	4	US-08-868-373-3
6	1478.5	65.7	1512	4	US-08-868-373-5
7	1282.5	57.0	1783	1	US-08-066-299-11
8	1282.5	57.0	1783	1	US-08-265-047-3
9	1263	56.1	1733	1	US-08-066-299-10
10	1263	56.1	1733	1	US-08-265-047-2
11	1263	56.1	1733	4	US-08-926-522-21
12	1249.5	55.5	1491	4	US-09-058-947A-3

13	1249.5	55.5	1502	4	US-08-868-373-11	Sequence 11, Appl
14	1249.5	55.5	1807	4	US-09-058-947A-2	Sequence 2, Appl
15	1249.5	55.5	3722	4	US-09-058-947A-1	Sequence 1, Appl
16	1242.5	55.2	1560	4	US-08-868-373-1	Sequence 1, Appl
17	1119	49.7	1650	4	US-08-868-373-7	Sequence 7, Appl
18	625.5	27.8	383	3	US-08-888-998-3	Sequence 3, Appl
19	625.5	27.8	383	3	US-09-362-633-3	Sequence 3, Appl
20	190	8.4	7198	4	US-08-994-035C-4	Sequence 4, Appl
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22	187	8.3	5076	4	US-08-494-907-2	Sequence 4, Appl
23	187	8.3	5076	5	PCT-US96-10986-2	Sequence 2, Appl
24	187	8.3	6170	5	US-08-494-907-4	Sequence 4, Appl
25	187	8.3	6170	5	PCT-US96-10986-4	Sequence 4, Appl
26	187	8.3	6387	5	US-08-494-907-3	Sequence 3, Appl
27	187	8.3	6387	5	PCT-US96-10986-3	Sequence 3, Appl
28	182.5	8.1	1047	2	US-08-494-907-11	Sequence 11, Appl
29	182.5	8.1	1047	5	PCT-US96-10986-11	Sequence 11, Appl
30	182.5	8.1	3680	2	US-08-494-907-1	Sequence 1, Appl
31	182.5	8.1	3680	5	PCT-US96-10986-1	Sequence 1, Appl
32	164.5	7.3	2728	3	US-08-836-402B-7	Sequence 7, Appl
33	156.5	7.0	23673	4	US-09-773-816-1	Sequence 1, Appl
34	155.5	6.9	747	5	PCT-US91-06234A-6	Sequence 6, Appl
35	155.5	6.9	1359	4	US-09-252-816A-2	Sequence 2, Appl
36	131	5.8	1485	1	US-08-471-601-23	Sequence 23, Appl
37	131	5.8	1485	1	US-08-474-556-23	Sequence 23, Appl
38	131	5.8	1485	1	US-08-479-382-23	Sequence 23, Appl
39	131	5.8	1485	1	US-08-470-354-23	Sequence 23, Appl
40	131	5.8	1485	1	US-08-479-383-23	Sequence 23, Appl
41	131	5.8	1485	2	US-08-479-041-23	Sequence 23, Appl
42	131	5.8	1485	4	US-08-819-646-23	Sequence 23, Appl
43	131	5.8	1485	4	US-09-195-716-23	Sequence 23, Appl
44	115.5	5.1	1002	4	US-09-134-001C-1109	Sequence 1109, Ap
45	114	5.1	1311	4	US-09-134-001C-1458	Sequence 1458, Ap

ALIGNMENTS

RESULT 1
US-08-888-998-1
; Sequence 1, Application US/0888998
; Patent No. 6124524
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: PAEL GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,998
; FILING DATE: 07-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,603
; FILING DATE: 26-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 12176-004300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:

LENGTH: 1641 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both

MOLECULE TYPE: cDNA
 FEATURE:

NAME/KEY: misc.feature

LOCATION: 1..1641

OTHER INFORMATION: /product- "FAEI from Arabidopsis"

US-08-888-998-1

Alignment Scores:

Pred. No.: 2,14e-226 Length: 1641
 Score: 2015.00 Matches: 385
 Percent Similarity: 93.75% Conservative: 20
 Best Local Similarity: 89.12% Mismatches: 27
 Indels: 0
 Gaps: 0

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 Db 283 GTCTCTAAGTCATGGATATTTCTACCAATTAAGAAAGCTGATCTTCACGGAAC 342
 QY 41 GlyThrCysAspAspSerTrpLeuAspPheLeuArgLysIleGlnIleArgSerGly 60
 Db 343 GTGGCATGTGATGATCGTCTCGTCGATTTCTTGAGGAAGATTCGAAGCGTTCAGGT 402
 QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
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 QY 81 AlaAlaAlaArgGluGluThrGluGlnValIleLeGlyAlaLeuGluAsnLeuPheLys 100
 Db 463 GCAGCGTCCAGTCAGAGACAGAGAAGGTATCATCGTGGCGCTCGAAATATTTCGAG 522
 QY 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
 Db 523 AACACCAAGTTAACCCCTAGAGAGATTGGTATATCTTGTGTGAATCAAGCATGTTTAA 582
 QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
 Db 583 CCNACTCCTTCGCTATCCGCTATGGTGTGTTAATCTTTCAAGCTCCGGAAGTACATCAA 542
 QY 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
 Db 643 AGCTTTAATCTAGGAGGAATCGGTGTAGTGTGTTTATTCGCAATGATTTGGCTAAA 702
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 Db 703 GACTTGTTCATGTTTCATTAACACTATGCTTGTGGTGGAGCTGAGACATCACA 762
 QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
 Db 763 CAAGGCATTTATGCTGGAGAAATAGATCAATGATGTTTAGCAATTTGCTGTTGTT 822
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 Db 823 GGTGGGCGCCGATTTTCTCTTAACAAGTCGGGACCGGAGACGTCCTCAAGTACAAG 882
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 QY 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
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 Db 1303 GCATACATAGAGCAAGGGAAGAAATGAAGAAGGAATAAAGCTTGGCAGATTGCTTTA 1362
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 Db 1423 GCAATAGTCTTGGCACTTGCATCGATAGATATCCGGTTAAATGATTGATCTGATTG 1482
 QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
 Db 1483 TCAAAGTCAAAGACTCATGTGCCAAAACGGTCGGTCC 1518

RESULT 2
 US-09-362-633-1
 ; Sequence 1, Application US/09362633
 ; Patent No. 6184355
 ; GENERAL INFORMATION:
 ; APPLICANT: JAMES, Douglas W.
 ; APPLICANT: LIM, Eda
 ; APPLICANT: KELLER, Janis
 ; APPLICANT: DOONER, Hugo K.
 ; TITLE OF INVENTION: FAEI GENES AND THEIR USES
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourile and Crew
 ; STREET: Stewart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94105-1493
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patencin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/362,633
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/888,998
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bastian, Kevin L.
 ; REGISTRATION NUMBER: 34,774
 ; REFERENCE/DOCKET NUMBER: 12176-004300

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1641
OTHER INFORMATION: /product= "FAE1 from Arabidopsis"
US-09-362-633-1

Alignment Scores:

Pred. No.: 2,14e-226 Length: 1641
Score: 2015.00 Matches: 385
Percent Similarity: 93.75% Conservative: 20
Best Local Similarity: 89.12% Mismatches: 27
Query Match: 89.56% Indels: 0
DB: 4 Gaps: 0

SEQ14-JOIN-SEQ4 (1-432) x US-09-362-633-1 (1-1641)

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DB 283 GTCTCTAAAGTCATGATATTTCTAGCAATAAGAAAGCTGATACCTTCTTCACGGAAC 342
QY 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnIleArgSerGly 60
DB 343 GTGCATGTGATGATCCGCTCCCTCGTCGATTTCTGAGGAGATCAAGACGCTACAGT 402
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DB 583 CCAACTCCTTCGCTATCCGCTATGCTGCTTAATACCTTCAAGCTCCGAGTAACATCAA 642
QY 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
DB 643 AGCTTTAATCTAGGAGGAATGGTGTAGTCTGGTGTATTGCCATTGATTTGGCTAAA 702
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DB 763 CAAGGCATTTATGCTGGAGAAATAGATCAATGATGCTGTAGCAATGCTTGTTCGTGTT 822
QY 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgArgSerLysTyrGln 220
DB 823 GGTGGGCGCGGATTTTGTCTCTCAACAGTCGGGAGACCGGAGACGCTCCAAAGTACA 882
QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
DB 883 CTAGTTCCACGCTCCGACGACATAGGAGCTGATGACAAGTCTTTTCGATGTGTGCAA 942

QY 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
DB 943 CAAAGAGCATGATGAGCGGCAAAATCGGAGTTTCTGTCTCAAAGACATAACCAATGTT 1002
QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
DB 1003 GCGGGACACACACTTACGAAAAATATAGCAACATGGGTGCGTGTCTCTCTTAAGC 1062
QY 281 GluLysLeuLeuPheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
DB 1063 GAAAGTTTCTTTTTCGCTACCTTCGCGCAAGAACTTCTAAAGGATAAAATCAAG 1122
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DB 1123 CATTAATGTTCCGGATTTCAAGCTTGTGTTGACCAATTTCTGTATTCATGCGGAGC 1182
QY 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
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QY 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTyrTyrGluLeu 360
DB 1243 TCTAGATCAACGTTACATAGATTGGGAATACTTCTCATCTAGCTCAATTTGGTATGATTA 1302
QY 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
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QY 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
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QY 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
DB 1423 GCAAATAGTCTTGGCAACATTCATCGATAGATATCGGTTAAATTCGGTTAAATTCGATTG 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
DB 1483 TCAAAGTCAAAGACTCATCTCCAAACACGTCGCTGCC 1518

RESULT 3

US-08-868-373-9
Sequence 9, Application US/08868373
Patent No. 6307128
GENERAL INFORMATION:
APPLICANT: Jaworski, Jan G.
APPLICANT: Post-Beittemmiller, Martha A.
APPLICANT: Todd, James
TITLE OF INVENTION: FATTY ACID ELONGASES
FILE REFERENCE: 07148/064001
CURRENT APPLICATION NUMBER: US/08/868,373
CURRENT FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 1611
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-08-868-373-9

Alignment Scores:
Pred. No.: 6,87e-169 Length: 1611
Score: 1524.50 Matches: 293
Percent Similarity: 81.45% Conservative: 45
Best Local Similarity: 70.60% Mismatches: 66
Query Match: 67.76% Indels: 11
DB: 4 Gaps: 2

SEQ14-JOIN-SEQ4 (1-432) x US-08-868-373-9 (1-1611)

QY 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerValSer 22
DB 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerValSer 22

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Db 397 GTTATCTCGTGTGTTACTCTGTTATCTCTCCGAGAGTCTTCAGGTTAAGTATCAG 456
Qy 23 LysValMetAspLeuPheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
Db 457 AAGTTTATGGATCATCTTAAGTTGATTAAGATTTCATAGTCAATCTCT----- 504
Qy 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeuGly 62
Db 505 -----TTAGATTTCAGAGGAGGATTCCTTGAAGCTTCGCTGTTTAGGA 546
Qy 63 AspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAlaAla 82
Db 547 GAAGAGACTTATCTCCCTGAAGCTTTACATTTATCCCTCCGAGGCTACGATGATGCG 606
Qy 83 AlaArgGluGluThrGluGlnValIleIleGlyAlaLeuAsnLeuPheLysAsnThr 102
Db 607 GCTCGTGAGGAACTCAGCAGGTAATGTTGCTCTCTGATTAAGCTTTTCGAGATACC 666
Qy 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122
Db 667 AAGATTAAACCTAGGATATTGCTGTTGTTGTTGTAATTGCTAGCTTGTAAATCCTACA 726
Qy 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
Db 727 CTTCTGCTGTCAGCTATGATTGTTAAACAGTATAAGCTTAGAGGATGTTT 786
Qy 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162
Db 787 AACCTTGTGCGAATGGGGTGATGCTGCTGCTGCTATCTCTATCGATTTAGTAAAGATATG 846
Qy 163 LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsn 182
Db 847 TTGCAAGTTCATAGGAATACCTATCTGCTGTTGTTAGTACTGAGAACATTAAGTATG 906
Qy 183 IleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGly 202
Db 907 TGGTATTGTTGGGAATAAGAGGCTATGTTGATCCGAATGTTGTTGCTGTTGGTGGT 966
Qy 203 AlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuVal 222
Db 967 TCGCGGATTTTGTGTCGAACAAGGGGAAAGATCGTAGACGGCTAAGTATAAGCTGTT 1026
Qy 223 HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGly 242
Db 1027 CATACCGTTAGGACTCATAAAGGAGCTGTTGAGAGGCTTTCAACTGCTGTTTACCAAGAG 1086
Qy 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
Db 1087 CAAGATGATAATGGAAGACCGGGTTTCGTTGTCGAAGATCTTATGGCTATAGCTGGG 1146
Qy 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLys 282
Db 1147 GAAGCTCTTAAGCGGAATATCACTACTTTAGGCTCTTGGTCTCTCCCTATAAGTGAGCAG 1206
Qy 283 LeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyr 302
Db 1207 ATTCTGTTTTTCACTTGTGTTACGAAGAACTGTTTAACTCGAAGCTGAAGCG --- 1263
Qy 303 TyrValProAspPheLysLysLeuAlaIleAspHisPheCysIleHisAlaGlyIlyArgAla 322
Db 1264 TATATCCGGATTTCAGGTTCCGGTTGATCTCTGTTAGGCTCTTGGTCTCTCCCTATAAGTGAGCT 1323
Qy 323 ValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342
Db 1324 GTGATTGATGAGCTGAGAAGAATCTGCAGCTTTTCGAGAGATCTATCTCGAGGCATCCAGA 1383
Qy 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrPheGluLeuAlaTyr 362
Db 1384 ATGACTGTCACAGATTTGGAACACTTCTTCGAGCTCGATTTGGTATGAACTGGCTTAC 1443
Qy 363 IleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGlySer 382
Db 1444 ATAGAGGCTAAGGTAGGATGAAGAAGAAACCGGGTTTGGCAGATTCTCTTTGGAGT 1503
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Qy 383 GlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThrAsn 402
Db 1504 GCGTTTAAAGTGAACAGTGCAGTTGGTGGCTCTAAACAATGTCAAGCCTTCGGTTAGT 1563
Qy 403 SerProTrpGluHisCysIleAspAspTyrProValLysIleAsp 417
Db 1564 AGTCCGTGGGAACACTGCTGCTGACCGATATCCGGTTTAGCTCGAC 1608

RESULT 4
US-08-868-373-13
: Sequence 13, Application US/08868373
: Patent No. 6307128
: GENERAL INFORMATION:
: APPLICANT: Jaworski, Jan G.
: APPLICANT: Post-Beittemmiller, Martha A.
: APPLICANT: Todd, James
: TITLE OF INVENTION: FATTY ACID ELONGASES
: FILE REFERENCE: 07148/064001
: CURRENT APPLICATION NUMBER: US/08/868,373
: CURRENT FILING DATE: 1997-06-03
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 13
: LENGTH: 1548
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-08-868-373-13

Alignment Scores:
Pred. No.: 4,85e-167 Length: 1548
Score: 1508.50 Matches: 285
Percent Similarity: 81.89% Conservatives: 54
Best Local Similarity: 68.67% Mismatches: 65
Query Match: 67.04% Indels: 11
DB: 4 Gaps: 3

SEQ14-JOIN-SEQ4 (1-432) x US-08-868-373-13 (1-1548)
Qy 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
Db 331 CCGCTTACTTGGTTGATTTCTCTGTTATCTCCACCTGATCATCTCAAGCTCCTTAC 390
Qy 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
Db 391 GCTCGGTTTCATG-----GAACATTCTAGACTCACCGGA 423
Qy 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
Db 424 GATTCGATGACTCTGCT---CTCGAGTTTCACGCAAGATCTCTGAGCGTTCTGGTTTA 480
Qy 62 GlyAspGluThrHisGlyProGlyLeuLeuGlnValProProArgLysThrPheAla 81
Db 481 GGGGAAGACACTTATGTCCTTGAAGCTATGCATTATGTTCCACCGAGAAATTCATGGCT 540
Qy 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
Db 541 GCTGCTAGAGAAGAGCTGAACAAGTCGTGTTGGTCTTAGATAACCTTTTCGCTAAC 600
Qy 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
Db 601 ACTAATGTGAACCAAGGATATTGGAATCCTTGTGTAATTTAGTCTCTCTTAATCCA 660
Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
Db 661 ACTCTCTGTTATCTGCANTGATTTGACACAGTATAGCTTAGAGGTATACATTAGAGC 720
Qy 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db 721 TACAATCTAGGCGGTATGGTTGTCAGCGGGAGTTATCGCTGCTGATCTTGTCAAGAC 780
Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
DB: 432
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Db 781 ATGTTGTTGGTACATAGGACACATTATCGGTTGTTGTTTCTACTGAGACATTACTCAG 840
Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
Db 841 AATGGTATTTGGTAAACAAGAAATCATGTTTATACCGAAGCTGCTTTTCGAGTTGGT 900
Qy 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 901 GGCTCGCGTTTGTCTATCGAACAAGTCGAGGGCAAGAGAGCGTCTAAGTCAGCGCTT 960
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 961 GTACATGTAGTCAGACATCCGCTGGAGCAGATGATAAGCTTCCTGGTTGTTTATCAA 1020
Qy 242 GlyAspAspLysGlyLysIleGlyValSerLysSerLysAspIleThrAspValAla 261
Db 1021 GAGCAGAGTATACAGAGGAAACCGGGTTCCTGTCGAAAGATCTAATGGCGATTGCA 1080
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
Db 1081 GGGAAACTCTCAAAACCAATATCATTACATTTGGGTCCTTTGTTCTACCGATAGTGAG 1140
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
Db 1141 CAGATTCTCTTCTTATGACTAGTTGTGAAGAAGCTCTTTAACCGTAAAGTGAACCG 1200
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArg 321
Db 1201 ---TATATCCGGATTCAAACTTGCCTTCGAGCATTTCTGATCCATCGCTGGTGGAGA 1257
Qy 322 AlaValIleAspValLeuGlyLysAsnLeuAlaLeuAlaProIleAspValIleAlaSer 341
Db 1258 GCTGTGATGATGAGTAGAGAAGAACTCGACGCTTCCACAGTTCATGTCGAGCTTCG 1317
Qy 342 ArgSerThrLeuHisArgPheLysAsnThrSerSerSerIleTyrTrpGluLeuAla 361
Db 1318 AGGATGACTTCATCGATTGGTAAACACATCTTCGAGCTCCATTTGTATGAATGGCT 1377
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
Db 1378 TACATTGAAGCAGGAGGAGGATGCGAAGAGGTAATCGTGTGGCAAAATCGCGTTCGGA 1437
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr 401
Db 1438 AGTGATTAAATGAATAGCGGATTTGGAGAGCATTAAGCATGTGAACCTTCGAAC 1497
Qy 402 AsnSerProTrpGluHisCysLysIleAspArgTyrProValLysIle 416
Db 1498 AACAGTCTTGGGAAGATTGTATTGACAAGTATCCGGTAACCTTTA 1542

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RESULT 5

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; US-08-868-373-3
; Sequence 3, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beitlenmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-3

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Alignment Scores:
Pred. No.: 3.4e-165 Length: 1479
Score: 1492.50 Matches: 282

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Percent Similarity: 81.62% Conservative: 60
Best Local Similarity: 67.30% Mismatches: 70
Query Match: 66.33% Indels: 7
DB: 4 Gaps: 3

SEQ14-JOIN-SEQ4 (1-432) x US-08-868-373-3 (1-1479)

Qy 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
Db 232 CCGGTTTATCTGTTAGCTTACTGCTACCTCCCGCTCGCATCTCAAGACCGACACC 291
Qy 22 SerLysValMetAspLysPheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41
Db 292 CAGAGGATCATCTAACACGCTTAAGCTTTGACGAGAAGCGCGCTGGAAGCA----- 345
Qy 42 ThrCysAspAspSerSerTrpLeu---AspPheLeuArgLysIleGlnGluArgSerGly 60
Db 346 -----GAGTCCGATTACTTGTGAGCTTCTCGGAGAAGATTTCTAGAACGTTCCGGT 396
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 397 CTAGGCCAAGAGAGCTAGTACCCGAAGGCTCTTCAAACTTTGCCACTTACACAGAAATTG 456
Qy 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 457 GCTGTATCACGTATAGAGACGAGAGGAGTTATTTGTCGGCTCGATATCTGTTCCG 516
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 517 AACACGGGAATCAACCCCTAGTATAGTATATTTGGTGGTGAATTCAGACACTTTTAT 576
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 577 CCAACACCTTCGCTATCAAGTATCTTAGTGAATAAGTTTAACTTAGGGATATATAAG 636
Qy 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 637 AGCTGGAATCTGGTGGGATGGGGTGTAGCGTGAGTCATCGCTATCGATCGGCTAAG 696
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 697 AGCTGTTTACAAGTTTCATAGAAACACTTATGCTTGTGGTGAGCAGGAGAACATCACT 756
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 757 CAAACTGTGATCGGTGTAACAACAATCAATGTTGGTTTCAAACTGTTTGTTCCTATA 816
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 817 GGTGGGCGCGGATTTTGTCTTCTAACCGGCTTATATAGATCTGTAACCGCAAAATACGAG 876
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 877 CTGTGTCACACCGTCCGGTCCATACCGGAGCAGATGACCGATCTATGAATGTGCAACT 936
Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 937 CAAGAAGAGATGAAGATGCGATAGTTGGGTTTCTTGTCTCAAGAATCTACCAATGGTA 996
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 997 GCTGCAAGAACCCATAAGATCAATATCGCAACTTTGGGTGCGCTGTGTTCTCCATAAGC 1056
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
Db 1057 GAGAAGTTTCACTTCTTGTGAGGTTCTGTTAAAGAAAGATTTCTCAACCCCAAGCTAAG 1116
Qy 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
Db 1117 CAT---TACATTCGGATTTCAGCTCGCATTCGAGCATTTCTGTATCCATCGCGGTGT 1173
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340

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Db 1174 AGAGCGCTAATTGATGAGATGGAGAGAATCTTCATCTCACTCACTAGACGCTTGAGGCT 1233
Qy 341 SerArgSerThrLeuHisArgPheGlyAenThrSerSerSerSerLeuTyrGluLeu 360
Db 1234 TCAGAATGACATTTACACAGGTTTGGTATATACCTCTTCGAGCTCCATTTGGTACGAGTTG 1293
Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysGlyAsnLysValTrpGlnIleAlaLeu 380
Db 1294 GCTTACAGAACCAAGGAGGATGACGAAGGAGATGGATTTGGCAGATTCGGTTG 1353
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer 400
Db 1354 GGGTCAGGTTTAAAGTGAATAGTTCAGTTTGGGTGGCTCTTCGTAACGTCGAAGCTTCT 1413
Qy 401 ThrAsnSerProTyrGluHisCysIleAspArgTyrProValLysIleAspSerAsp 419
Db 1414 ACTAATATCTCTGGGAACAGTGTCTACACAAATATCCAGTTGAGATCGATATAGAT 1470
RESULT 6
US-08-868-373-5
; Sequence 5, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-beittemillier, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868.373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-5
Alignment Scores:
Pred. No.: 1,54e-163 Length: 1512
Score: 1478.50 Matches: 280
Percent Similarity: 81.97% Conservative: 61
Best Local Similarity: 67.31% Mismatches: 72
Query Match: 65.71% Indels: 3
DB: 4 Gaps: 2
SEQ14-JOIN-SEQ4 (1-432) x US-08-868-373-5 (1-1512)
Qy 2 ProValTyrLeuValAspTyrSerCystTyrLeuProProHisLeuArgValSerVal 21
Db 271 CCCGTTTACCTTGTGATTTCTCTGCTACCTTCCACCGTCGCATCTCAAGGTCAGTATC 330
Qy 22 SerLysValMetAspPheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
Db 331 CAACCCCTAATGGGACCCACGACGTCGACAGAGAACGATGTGTGGGAAGAACAA 390
Qy 42 ThrCysAspSerSerTyrLeuAspPheLeuArgLysIleGlnIleArgSerGlyLeu 61
Db 391 GAGAGCGAC-----CATTTAGTTGACTTCCAGGAGAGATTTCTGACAGTTCCGGTCTT 444
Qy 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProArgLysThrPheAla 81
Db 445 GGTCAAGAACCTTACATCCCGAGGGTCTTCAGTGCTTCCCATCTCAGCAAGCATGGGT 504
Qy 82 AlaAlaArgGluThrGlnValIleIleGlyAlaLeuGluAsnValLysAsn 101
Db 505 GCTTCAGGTAAGAGAGCGAAGCAAGTAATCTTCGGAGCTCTTCGACAATCTTTTCGCAAC 564
Qy 102 ThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnPro 121
Db 565 ACCGGTGAACCTGATATCGGTATTTGGTGTGTAATCTAGACACGTTTAATCCA 624
Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
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Db 625 ACTCCATCACTCCCTCCATGATTTGAACAAGTACAAAACCTCAGACACAACATCAAGAT 684
Qy 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db 685 TTGAATCTTGGAGGATGGTTGCAGTCCCGAGTTTATAGCTTTGATGTCGCTCAAGGGA 744
Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValIleSerThrGluAsnIleTyr 181
Db 745 TTACTACAAGTTTCATAGGAACACTTATGCTATTGTAGTAAAGCACAGAACATCACTCAG 804
Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
Db 805 AACTTATCTTGGGAAAAACAATCAATGCTAGTCAAACTGTTTGTCCCGCTGGT 864
Qy 202 GlyAlaAlaIleLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 865 GGTGCTCGGTTCTGCTTTCAACAGATCTAGACCGTTAACCGCGCCAAATACGAGCTT 924
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 925 GTTCACACCGTACGATCCATACCGGATCAGATGATAGTCTTTCGAATGTCGACACAA 984
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db 985 GAAGAGGATCAAGATGGTATAATTTGGAGTTACCTTGACAAAGAAATCTACCTATGCTG 1044
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
Db 1045 GCAAGGACTCTTAAGATAAATATCGCAACTTTGGGTCTCTGTACTTCCATTAAAGAG 1104
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
Db 1105 ARGCTAGCCTCTTTATTACTTTTTCAGAGAAGATATTTCAGCCAGAGTTAAGGAAT 1164
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArg 321
Db 1165 ---TATACACACAGATTTCAAGCTTTGCGCTTTGAGCATTTCTGTATCCAGCTGTGGAAGA 1221
Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db 1222 GCTCTAATAGTACGCTGGAGAAGACCTTAAGCTTTCTCCGTTACACGTAGAGGGGTCA 1281
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTyrTyrGluLeuAla 361
Db 1282 AGAATGACACTACACAGGTTTGGTAACACTTCTTCTAGCTCAATCTGTGACGAGTAGCT 1341
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
Db 1342 TATACAGAAGCTTAAAGGAGGATGAAGAGGAGATGAGGATTTGGCAGATTTGTTGGGG 1401
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr 401
Db 1402 TCAGGTTTAAAGTGAACAGTTCAATATGGTGGCTCTCCGAGACGTTAAGCCTTCAGCT 1461
Qy 402 AsnSerProTyrGluHisCysIleAspArgTyrProValLysIleAsp 417
Db 1462 AACAGTCCATGGGAAGACTGTATGGATAGATATCCGGTTGAGATTGAT 1509
RESULT 7
US-08-066-299-11
; Sequence 11, Application US/08066299
; Patent No. 5445947
; GENERAL INFORMATION:
; APPLICANT: James George Metz
; APPLICANT: Kathryn Dennis Lardizabal
; APPLICANT: Michael W. Lassner
; TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol
; NUMBER OF INVENTIONS: O-Acyltransferases
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
```

CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 6.0.7
 SOFTWARE: Microsoft Word 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/066,299
 FILING DATE: 19930520
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/796,256
 FILING DATE: 20-NOVEMBER-1991
 APPLICATION NUMBER: 07/933,411
 FILING DATE: 21-AUGUST-1992
 APPLICATION NUMBER: PCT/US92/09863
 FILING DATE: 13-NOVEMBER-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 REFERENCE/DOCKET NUMBER: CGNE 98
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-066-299-11

Alignment Scores:

Pred. No.: 1,93e-140 Length: 1783
 Score: 1282.50 Matches: 246
 Percent Similarity: 75.66% Conservative: 68
 Best Local Similarity: 59.28% Mismatches: 90
 Query Match: 57.00% Indels: 11
 Ds: 1 Gaps: 3

SEQ14-JOIN-SEQ4 (1-432) x US-08-066-299-11 (1-1783)

QY 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerValSer 22
 DB 334 GTCTACTGTGGTACCTTCCCTGCTATAGCCCTCACCCGACCTGATACATCCACGAG 393
 QY 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
 DB 394 ATGTTCTAGT-----GACCGACCTCCCGCGCGGGTGG 426
 QY 43 CysAspSerSerTyrLeuAspPheLeuArgLysIleGlnIleArgSerGlyLeuGly 62
 DB 427 TTTTCTAAGGAGAT---ATTGAGTTTCAGAGAGAGATCTTGAGAGGCGCGGTATGGGC 483
 QY 63 AspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAlaAla 82
 DB 484 CGGGAACCTTACCTCCCGAATCCGTCCTACTAAGGTGCGCGCGCGAGCATAGCAGCA 543
 QY 83 AlaArgGluThrGlnValIleGlyAlaLeuGlnValLeuLeuPheLysAsnThr 102
 DB 544 GCCAGGCCGAGCGGAGGAGGTGTGTACGGGCGGATGACGAGGTGTGTGGAGAGACG 603
 QY 103 AsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnProThr 122
 DB 604 GGGGTGAAGCCGAGCAGATAGTAATCTGTGTGTAACCTTGTGTTAAACCAACG 663
 QY 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142

DB 664 CCGTCGCTGTCATCCATGATAGTTAACCATTTACAAGCTTAGGGGTATATATACCTAT 723
 QY 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162
 DB 724 AATCTTGTGGCATGGTTCAGCTGCTGGCTCATTTCCATTGATCTTGCACAGGACCTC 783
 QY 163 LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsn 182
 DB 784 CTACAGGTTTACCCTAACATATGTTAGTAGTGACGACAGAAACATGACCCCTAAT 843
 QY 183 IleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 202
 DB 844 TGGTACTGGGCAATGACCGCTCATGCTTATACCAACTGCCTATTTCATCGGTGGC 903
 QY 203 AlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuVal 222
 DB 904 GCTGCATCATCTCTCAAAACCGCTGGCGTGATCGTCCGATCCAAAGTACCACTCCCT 963
 QY 223 HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGly 242
 DB 964 CACACAGTACGCCACCAAGGCGCTGACGACAGTCTTATAGATCGCTTACACAA 1023
 QY 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
 DB 1024 GAAGATGAATTAACAAGGTAGGTGTGCTTATCCAGGATCTGATGGCGGTGGCGGT 1083
 QY 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLys 282
 DB 1084 GAAGCCCTAAAGGCCAACATCAGACCCCTTGGTCCCTCGTCCCTCCCATGTGAGAACAA 1143
 QY 283 LeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyr 302
 DB 1144 CTCCTCTTCTTGGCCACCTTAGTGGCACGTAAAGTCTTCAAGATGACGACGTAAGCA 1203
 QY 303 TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArgAla 322
 DB 1204 TACATCCAGATTTCAAGTTGGCAGCGAAGCACTTCTGCATCCATCGAGGAGCAAGCA 1263
 QY 323 ValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342
 DB 1264 GTGTGGATGAGCTCGAGACGACTTGGAGTTGACGCGCTGGACCTTGACCCCTCGAGG 1323
 QY 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeuAlaTyr 362
 DB 1324 ATGACACTGTATAGTTTGGGAAACACATCGATGCTCATTTATGTTAGGATGGCATAC 1383
 QY 363 IleGluAlaLysGlyArgMetLysLysGlyAsnLysValTyrGlnIleAlaLeuGlySer 382
 DB 1384 GCTGAAGCAAAAGGAGGATCCGTAGGGGTGATCGAATCTGGATGATGGATTGGTTCA 1443
 QY 383 GlyPheLysCysAsnSerAlaValTyrValAlaLeuAsnAsnValLys---AlaSerThr 401
 DB 1444 GGTTCAGTGTAAACAGTGTGTGTGGAGGGCTTTGAGGAGGTGCAATCGCGGTAGAGAG 1503
 QY 402 AsnSerProTyrGluHisCysIleAspArgTyrProValLysIle 416
 DB 1504 ARAATCTCTGGATGATGAATTTGAGATTTCCCTGTCCATGTG 1548

RESULT 8

US-08-265-047-3
 Sequence 3, Application US/08265047
 Patent No. 5679881

GENERAL INFORMATION:

APPLICANT: Metz, James G.
 APPLICANT: Lardizabal, Kathryn D.
 APPLICANT: Lassner, Michael
 TITLE OF INVENTION: Nucleic Acid Sequences Encoding a Plant Cytoplasmic Protein
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis

```

STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,047
FILING DATE: 23-JUN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/160,602
FILING DATE: 30-NOV-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/796,256
FILING DATE: 20-NOV-91
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/933,411
FILING DATE: 21-AUG-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/066,299
FILING DATE: 20-MAY-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09863
FILING DATE: 13-NOV-92
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 101-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-265-047-3

Alignment Scores:
Pred. No.: 1.93e-140 Length: 1783
Score: 1282.50 Matches: 246
Percent Similarity: 75.66% Conservative: 68
Best Local Similarity: 59.28% Mismatches: 90
Query Match: 57.00% Indels: 11
Dbs: 1 Gaps: 3

SEQ14-JOIN-SEQ4 (1-432) x US-08-265-047-3 (1-1783)
QY 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerValSer 22
Db 334 GTCTACTGGTGGACITTCCTGCTATTAAGCCTCACCGAACTGTATACATCCCAACGAG 393
QY 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
Db 394 ATGTTTCATG-----GACCGGACCTCCCGGGCGGGTGG 426
QY 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeuGly 62
Db 427 TTTTCTAGGAGAT---ATTGAGTTTCAGGAGAGATCTTGGAGAGGCCGGGTATGGGC 483
QY 63 AspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAlaAla 82
Db 484 CGGGAACCTACGTCCTCCGAATCCGTCACCTAAGGTGGCCGCCCGGAGCCGAGCATGACGA 543

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QY 83 AlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThr 102
Db 544 GCCAGGCCCGAGCGAGGAGGTGTGTACGGCGCATGACGAGGTGTGTGAGAGACG 603
QY 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122
Db 604 GGGGTGAAGCCGAGACAGATAGGAATACTGGTGTGAACCTGTCAGCTTGTATACCCACG 663
QY 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
Db 664 CCCTCGCTGTCTCATCATGATGATTAACCATTAACAAGCTTAGGGGTAATATATCTAGCTAT 723
QY 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162
Db 724 AATCTTGGTGGCATGGTGTGAGTGTGCTGGGCTCATTTCCATGATCTTGCCACAGACCTC 793
QY 163 LeuHisValHisLysAsnThrTrpAlaLeuValValSerThrGluAsnIleThrTyrAsn 182
Db 784 CTACAGTTTACCGTAACACATATGTGTAGTAGTGAGCAGACAGAAACATGACCCCTTAAT 843
QY 183 IleTyrAlaGlyAspAsnArgSerMetMetValSerAspCysLeuPheArgValGlyGly 202
Db 844 TGGTACTGGGCAATGACCGCTCCATGCTTATCACCACCTGCTATTTCCGATGGGTGGC 903
QY 203 AlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuVal 222
Db 904 GCTGCCATCATCTCTCAACCGCTGGCGTGTGCTGCGCGATCCCAAGTACCAACTCCTT 963
QY 223 HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGly 242
Db 964 CACACAGTACGCCACCAAGGCGCTGACGACAGTCTATAGATGCGTCTTACACAA 1023
QY 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
Db 1024 GAGATGAAATAACAAAGGTAGGTGGTTCCTTATCAAGGATCTCATGCGCATGGCGGT 1083
QY 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlyLys 282
Db 1084 GAAGCCCTAAAGCCCAACATCAGCAGCTTGGTCCCTCGTCTCCCTCCCATGTCAGACAA 1143
QY 283 LeuLeuPhePheValThrPheMetGlyLysLeuPheLysAspLysIleLysHisTyr 302
Db 1144 CTCTCTCTTTTGGCCACCTTAGTGGCAGCTAAGTCTTCAAGATGACGACGTGAAGCCA 1203
QY 303 TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArgAla 322
Db 1204 TACATCCAGATTTCAAAGTTGGCAGCGAAGCACTTCTGCATCCATGACGAGGCAAGCA 1263
QY 323 ValIleAspValLeuGlyLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342
Db 1264 GTTGTGATGAGCTCGAGACGAACTTGGAGTTGACGCCATGGCCATGGACCTTGAACCTCGAGG 1323
QY 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTrpTyrGluLeuAlaTyr 362
Db 1324 ATGACACTGTATAGTTTGGGAACACATCGAGTAGCTCATTTATGTTAGGAGTTGGCATAC 1383
QY 363 IleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGlySer 382
Db 1384 CTTGAAGCAAAAGGAGGATCCGTAAGGGGTGATCGAACTTGGATGATTTGGATTGGTTTCA 1443
QY 383 GlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLys---AlaSerThr 401
Db 1444 GGTTTCAAGTGAACAGTGTGTGTGGAGGCTTTTGAGGAGGTGTCAATCCGCGCTAGAGAG 1503
QY 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIle 416
Db 1504 AAGATCCCTTGGATCGATGAAATTTGAGAATTTCCCTGTCCATGTG 1548

```

RESULT 9

US-08-066-299-10

; Sequence 10, Application US/08066299

; Patent No. 5445947

GENERAL INFORMATION:

APPLICANT: James George Metz
 APPLICANT: Kathryn Dennis Lardizabal
 APPLICANT: Michael W. Lassner
 TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol
 TITLE OF INVENTION: O-Acyltransferases
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 6.0.7
 SOFTWARE: Microsoft Word 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/066,299
 FILING DATE: 19930520
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/796,256
 FILING DATE: 20-NOVEMBER-1991
 APPLICATION NUMBER: 07/933,411
 FILING DATE: 21-AUGUST-1992
 APPLICATION NUMBER: PCT/US92/09863
 FILING DATE: 13-NOVEMBER-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 REFERENCE/DOCKET NUMBER: CGNE 98
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1733 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cdna to mRNA
 US-08-066-299-10

Alignment Scores:

Pred. No.: 3,56e-138 Length: 1733
 Score: 1263.00 Matches: 245
 Percent Similarity: 75.24% Conservative: 68
 Best Local Similarity: 58.89% Mismatches: 91
 Query Match: 56.13% Indels: 12
 Gaps: 4

SEQ14-JOIN-SEQ4 (1-432) x US-08-066-299-10 (1-1733)

QY 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerValSer 22
 DB 369 GTCTACTTGTGGACCTTGGATGCTATTAAGCTCAACCGAACCTGTGATCCACGAG 428
 QY 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
 DB 429 ATGTTTCATG-----GACCGACCTCCCGGGCGGGTGG 461
 QY 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeuGly 62
 DB 462 TTTTCTAAGGAGAT---ATTGAGTTTCAGAGGAGAGATCTTGGAGAGGCCGGGTATGGGT 518
 QY 63 AspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAlaAla 82
 DB 519 CGGGAACCTATGTCGCCGATCCGTCCTACTAAGGTGTCGCCGAGCGGCGGATAGCAGA 578

QY 83 AlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThr 102
 DB 579 GCCAGGCCGAGCGGAGGAGGTGATGTACGGGCGATCGACGAGGTGTGGAGAACG 638
 QY 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122
 DB 639 GGGGTGAAGCGGAGCAGATAGTAATCTGTTGGTGACTGCGAGCTGTGTTAACCAACG 698
 QY 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
 DB 699 CCGTCGCTGTCATCCATGATAGTTAAACCATTAAGCTNAGGGGTAAATATCTAGCTAT 758
 QY 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162
 DB 759 AATCTTGGTGGCATGGTGTGCTGCTGGCTCATTTCCATTGATCTTGCAAGGACCTC 818
 QY 163 LeuHisValHis---LysAsnThrTyrAlaLeuValSerThrGluAsnIleThrTyr 181
 DB 819 CTACAGGTTTACCCTAAACACATATGTTAGTAGTGACGACGGAACATGACCCCTT 878
 QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 DB 879 AATTGGTACTGGGCAATGACCGCTCATCTATATACCAACTGCCTATTTCGCTGGGT 938
 QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
 DB 939 GCGCTGCCATCATCTCTCAACCCCTGGCTGATCGCCGATCCAGTACCAAGTACCACTC 998
 QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
 DB 999 CTTTCATACAGTACGACCCCAAGGGCGCTGACGACAAAGTCTCTATAGATCGCTTACAA 1058
 QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
 DB 1059 CAAGAAGATGAATAACAAGTAGGTGCTTATCCAAGGATCGTGGCAGTGGC 1118
 QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
 DB 1119 GGTGAAGCCCTAAAGGCGCAACATCAGGACCCCTGGTGGCTCCCTCGCTCCCATGTG 1178
 QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
 DB 1179 CAACTCCTCTCTTGGCCACCTTAGTGGCAGCTAAGGTCTTCAAGATGACGACGTAAG 1238
 QY 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArg 321
 DB 1239 CCATACATCCCGAGATTTCAAGTTGGCAGCGACGACTTCTGCATCCATGCGAGGACAA 1298
 QY 322 AlaValIleAspValIleGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
 DB 1299 GCAGTGTGGATGACCTCGAGAGAACTTGGAGTTGACGCCCATGGCACCTTGACCTCG 1358
 QY 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleThrTyrGluLeuAla 361
 DB 1359 AGGATGACACTGTATAGTTTGGGAACACATCCAGTAGCTCATTTAGTGTACGAGTTGG 1418
 QY 362 TyrIleGluAlaLysGlyArgMetLysLysAsnLysValTrpGlnIleAlaLeuGly 381
 DB 1419 TAGCCTGAAGCAAAAGGAGGAGTCCCGTAAGGTGATCGAACTTGGATGATTGGATTGGT 1478
 QY 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLys---AlaSer 400
 DB 1479 TCAGGTTCAAGTGAACAGTGTGTGGAGGGCTTGGAGAGGTGTCATCGCGCTAGA 1538
 QY 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIle 416
 DB 1539 GAGAAGAATCCTTGGATGATGAATTAAGAAAGTTGAGAAAGTTCCCTGTCCATGTG 1586

RESULT 10

US-08-265-047-2
 ; Sequence 2, Application US/08265047
 ; Patent No. 5679881


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Db 1479 TCAGGTTTCAAGTGTAAACAGTGTCTGTGGAGGCGCTTTGAGGAGTGTCAATCCGGCTAGA 1538
Qy 401 ThrAnSerProTrpGluHisCysIleAspArgTyrProValLysIle 416
Db 1539 GAGAAGAATCCTTGGATGATGAAATTTGAGAAGTTCCCTGTCCATGTG 1586
RESULT 11
US-08-926-522-21
; Sequence 21, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vic C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,522
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,173
; FILING DATE: 2-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CENE DES
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-926-522-21
Alignment Scores:
Pred. No.: 3,566-138 Length: 1733
Score: 1263.00 Matches: 245
Percent Similarity: 75.24% Conservative: 68
Best Local Similarity: 58.89% Mismatches: 91
Query Match: 56.13% Indels: 12
DB: 4 Gaps: 4
SEQ14-JOIN-SEQ4 (1-432) x US-08-926-522-21 (1-1733)
Qy 3 ValTyrLeuValAspTyrSerCysIleLeuProHisLeuArgValSerValSer 22
Db 369 GTCTACTTGGTGGACCTTGGATGCTATTAAGCTCAACGAACTGATGACATCCACGAG 428
Qy 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
Db 429 ATGTTTCATG-----GACCGGACCTCCCGGGCGGGTCG 461
Qy 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnLysLeuGlyLeuGly 62
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Db 462 TTTTCTAAGGAGAAT--ATTGAGTTTTCAGAGCAAGATCTTTGGAGAGGCGCGGTATGGGT 518
Qy 63 AspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAlaA1a 82
Db 519 CGGGAACCTATGTCCTCGAATCCGTCACCTAAGGTGCCCGGAGCCGAGCAGCAGTAGCAGCA 578
Qy 83 AlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluGlnLeuPheLysAsnThr 102
Db 579 GCCAGGGCGGAGGAGGAGGTGATGTACGGCGCATCGACAGGTGTTGGAGAGAGCG 638
Qy 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122
Db 639 GGGGTGAAGCCGAGCAGATAGTAAGTCTGGTGGTGAAGTCTGCTTTAACCCCAAGC 698
Qy 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
Db 699 CGTGTGCTGTATCATCATGATAGTTAACCATTTACAGCTNAGGGGTAATATATATCTAT 758
Qy 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162
Db 759 AATCTTGGTGCGATGGGTGCGAGTCTGGGCTCATTTCCATTGATCTTGCCAGGACCTC 818
Qy 163 LeuHisValHis---LysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
Db 819 CTACAGTTTACCCTAAACACACATATGTGTAGTAGTAGCAGCGGAAACATGACCCCT 878
Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
Db 879 AATTGTACTGGGCAATGACCGCTCCATGCTTATCACCACCTGCTATTTCCGATGGGT 938
Qy 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 939 GGGCTGCGCATCATCTCTCAACCGCTGGCGTGGTGTGTCGCGCATCCAGTACCACTC 998
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 999 CTTTCATACAGTACGCCACCCACCAAGGGCGCTGACGACAGTCTCTATAGATGCTGTACAA 1058
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db 1059 CAAGAAGATGAAATAACAGGTAGGTGTGCTTATCCAGGATCTGTATGGCGAGTTGGCC 1118
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
Db 1119 GGTGAAGCCCTAAAGGCCAACATCAGCAGCCCTTGGTCCCTGCTGCTCCCATCTCAGAA 1178
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
Db 1179 CAATCTCTCTTTGCGCACCTTAGTGGCACGTAAGTCTTCAAGATGACGACGCTGAAG 1238
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyIleArg 321
Db 1239 CCATACATCCAGATTTCAAGTTGGCAGCGACGACTTCTGTCATCCATCGAGGAGGCAAA 1298
Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db 1299 GCAGTGTGTGATGACCTCGAAGAACTTGGAGTTCACCCCATGGCCACCTTGAACCCCTCG 1358
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeuAla 361
Db 1359 AGGATGACACTGTATAGGTTTGGGAACACATCGAGTAGCTCATTTATGTTAGGAGTTGGCA 1418
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
Db 1419 TAGCTGAAGCAAAAGGAGGATCCGTAAAGGGTGTGCAACTTGGATGATGATTTGGT 1478
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLys---AlaSer 400
Db 1479 TCAGGTTTCAAGTGTAAACAGTGTGTGTGGAGGCTTTGAGGAGTGTCAATCCGGCTAGA 1538
Qy 401 ThrAnSerProTrpGluHisCysIleAspArgTyrProValLysIle 416
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Db 1539 GAGAGAATCCTTGGATGATGAAATTGAGAAAGTTCCCTCCCTGTCATGNG 1586

RESULT 12

US-09-058-947A-3

; Sequence 3, Application US/09058947A

; Patent No. 6274790

; GENERAL INFORMATION:

; APPLICANT: Kunst et al.

; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme

; TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klarquist Sparkman Campbell

; ADDRESSEE: Leigh & Whinston, LLP

; STREET: One World Trade Center, Suite

; STREET: 1600, 121 S.W. Salmon Street

; CITY: Portland

; STATE: OR

; COUNTRY: USA

; ZIP: 97204-2988

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disk, 3.5-inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows NT

; SOFTWARE: Word97 & ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/058,947A

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/043,831

; FILING DATE: April 14, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: David J. Earp, Ph.D.

; REGISTRATION NUMBER: 41,401

; REFERENCE/DOCKET NUMBER: 5493-50032/DJE

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 226-7391

; TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1491

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-09-058-947A-3

Alignment Scores:

Pred. No.: 1.08e-136 Length: 1491

Score: 1249.50 Matches: 237

Percent Similarity: 73.43% Conservative: 67

Best Local Similarity: 57.25% Mismatches: 99

Query Match: 55.53% Indels: 11

DB: 4 Gaps: 2

SEQ14-JOIN-SEQ4 (1-432) x US-09-058-947A-3 (1-1491)

QY 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerValSer 22

Db 265 ATCTACCTCGTTGACTATTCTTGTACAGCCACCTGTCAGGTGCTGCTCCCTTCGCA 324

QY 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42

Db 325 ACTTTCATGGAACTCTCTGTTGATCCTCAAG----- 357

QY 43 CysAspAspSerSerTrpLeuArgLysIleGlnLeuArgSerGlyLeuGly 62

Db 358 --GACAAGCCTAAGACCGTCGAGTTCCAAATGAGAACTCTTGAACGTTCTGCGCTCGGT 414

QY 63 AspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAlaAla 82

Db 415 GAGGAGACTTCTCTCCCGCTATTCATTTATATTCCTCCCAACCAACCATGGACGCG 474

QY 83 AlaArgGluGluThrGluGlnValIleIleGlyAlaLeuLeuAsnLeuPheLysAsnThr 102

Db 475 GCTAGAAGCGAGCGCTCAGATGTTATCTTCGAGGCCATGAGCATCTTTTCAAGAAACC 534

QY 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122

Db 535 GGTCTTAAACCTAAAGACGTCGACATCCTTATCGTCAACTGCTCTCTTTCTCTCCACA 594

QY 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142

Db 595 CCATCGCTCTCAGCTATGCTCATCAACAATATAGCTTAGGAGTAATATCAAGAGCTTC 654

QY 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162

Db 655 AATCTTTCCGGGATGGCTGCAGCGCGGCTGATCTCAGTTGATCTAGCCCGGACTTG 714

QY 163 LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsn 182

Db 715 CTCCAAGTTTCATCCCAATTCAAATGCAATCATCGTCAGCAGGAGATCATACGCCCTAAT 774

QY 183 IleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGly 202

Db 775 TACTATCAAGGCCAACGAGAGAGCCATGTTGTATCCCAATGTCTCTCCGCATGGGTGCG 834

QY 203 AlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuVal 222

Db 835 GCAGCCATACATGTCAAACCGCGGCTGACCGGTGGCGGAGCCCAATACAGCTTCC 894

QY 223 HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGly 242

Db 895 CACCTCTCGGACACACCGTGGCGCTGACGACAAGTCTTTCTACTGTGTCTACGACAG 954

QY 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262

Db 955 GAGACAAGAGAGACGCTGGCATCACTGTCCAAAGATCTCATGGCCATGGCGGT 1014

QY 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlyLys 282

Db 1015 GAAGCCCTCAAGGCCAAACATCACCACAATAGGTCCTTGTGCTCTACCGCGTCAGAACAA 1074

QY 283 LeuLeuPhePheValThrPheMetGlyLysLeuPheLysAspLysIleLysHisTyr 302

Db 1075 CTTCCTCTCTCAGTCCCTAATCGGAGCTAAATCTTCAACCCCAATGGAAACCA--- 1131

QY 303 TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAla 322

Db 1132 TACATACCGGATTTCAAGCTGGCCTTCGAACTTTTGCATTCAGCGAGGAGCGAGCG 1191

QY 323 ValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342

Db 1192 GTGATCGAGAGCTCCAAAGANANTCTACACTATCAGGAGACACGTTGAGGCTCANGA 1251

QY 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTrpTyrGluLeuAlaTyr 362

Db 1252 ATGACACTACATCGTTTGGTAACACGCTCATCTCTATCGTTATGTTAGCAGCTTAGCTAC 1311

QY 363 IleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGlySer 382

Db 1312 ATCAGTCTAAAGGAGAGATGAGGAGGCGATCGGCTTGGCAATCCGCTTGGGAGT 1371

QY 383 GlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThrAsn 402

Db 1372 GGTTCAGATGTAACCTCTGCGGTGGAAATGTAACCGTACGATTAAGACACCTAAGGAC 1431

QY 403 SerProTrpGluHisCysIleAspArgTyrProValLysIle 416

Db 1432 GGACCATGGTCCGANTGTATCGCCGTATACCCGTCTCTTATT 1473

RESULT 13

US-08-868-373-11

; Sequence 11, Application US/08868373

; Patent No. 6307128

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Post-Beittemmiller, Martha A.
 ; APPLICANT: Todd, James
 ; TITLE OF INVENTION: FATTY ACID ELONGASES
 ; FILE REFERENCE: 07148/064001
 ; CURRENT APPLICATION NUMBER: US/08/868,373
 ; CURRENT FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 11
 ; LENGTH: 1502
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-08-868-373-11

Alignment Scores:

Pred. No.: 1,09e-136 Length: 1502
 Score: 1249.50 Matches: 237
 Percent Similarity: 73.43% Conservative: 67
 Best Local Similarity: 57.25% Mismatches: 99
 Query Match: 55.53% Indels: 11
 DB: 4 Gaps: 2

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 QY 23 LysValMetAspTyrPheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
 DB 334 ACTTTCATGGAACACTCTCGTTGATCTCTCAAG----- 366
 QY 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnLeuArgSerGlyLeuGly 62
 DB 367 ---GACAGCCCTAAGAGCTGAGTGTCCAAATGAGAACTCTGACGCTTGGCGCTCGGT 423
 QY 63 AspGlnThrHisGlyProGluGlyLeuLeuValProProArgLysThrPheAlaAla 82
 DB 424 GAGGAGACTTGTCCTCCCTCCGCTATTCAATATATCTCTCCACCAACCACTGAGCGG 483
 QY 83 AlaArgGluGlnThrGlnValIleGlnValLeuGlnValLeuGlnValLeuGlnValSer 102
 DB 484 CTAAGAGCCGAGCTCAGATGTTATCTTCGAGCCATGAGCATCTTTTCAAGAAACC 543
 QY 103 AsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnProThr 122
 DB 544 GGTCTTAACCTAAAGACGTCGACATCTTATCTCAACTGCTCTCTCTCTCTCCACA 603
 QY 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
 DB 604 CCATCGCTCTACGATGTCATCAACAAATATATAGCTTAGGNTATATCAAGAGCTTC 663
 QY 143 AsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162
 DB 664 AATCTTTTGGGGATGGGCTGACGCGGGCTGATCTCACTGATGATCAAGCCGAGCTTG 723
 QY 163 LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGlnAsnIleThrTyrAsn 182
 DB 724 CTCCAAGTTCATCCCAATCAATCAATCATCTGTCAGCAGGAGATCAATCAATCAAT 783
 QY 183 IleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGly 202
 DB 784 TACTATCAAGGCAACGAGAGCCATGTTTATCCCAATTTGCTCTCTCGCATGGGTGCG 843
 QY 203 AlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuVal 222
 DB 844 GCAGCCATACATATGTCACACCGCGGCTGACCGGGTGGGAGCCAAATCAAGCTTTC 903
 QY 223 HisThrValArgThrHisThrGlnAlaAspGlyLysSerPheArgCysValGlnGlnGly 242
 DB 904 CACCTCGCTCCGGACACACCGCTGCTGACGACAAGTCTTCTACTGTGCTCTACGAACAG 963

QY 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
 DB 964 GAAGACAAGAGGACACAGTGGCATCACTTGTCCAAAGATCTCATGGCCATGCGCGGT 1023
 QY 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSerGluLys 282
 DB 1024 GAAGCCCTCAAGGCAACATCACCAATAGTCTCTTTGGTCTTACCGGCGTCAGAACAA 1083
 QY 283 LeuLeuPhePheValThrPheMetGlyLysLeuPheLysAspLysIleLysHisTyr 302
 DB 1084 CTTCCTCTCTCAGTCCCTAATCGGAGCTAAATCTTCAACCGGAATGGAACCA--- 1140
 QY 303 TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyAla 322
 DB 1141 TACATACCGGATTTCAAGCTGGCTTCGAACACTTTTCATTCACGAGGAGGAGCG 1200
 QY 323 ValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342
 DB 1201 GTGATCGAGAGCTCCAAAGAAATCTCAACTATCGAGGAACACGTTGAGGCTCAAG 1260
 QY 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTyrGluLeuAlaTyr 362
 DB 1261 ATGACACTACATCTGTTTGGTAACAGCTCATCTTCATCGTTATGTTACGAGCTTAC 1320
 QY 363 IleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGlySer 382
 DB 1321 ATCGAGTCTAAGGAGAAATGAGGAGGCGATCGCTTGGCAATCGCGTTGGAGT 1380
 QY 383 GlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThrAsn 402
 DB 1381 GGTTCAAAGTGAACCTCGCTGCGGTGGAAGTGAACCGTACGATTAAGACACCTAAG 1440
 QY 403 SerProTrpGluHisCysIleAspArgTyrProValLysIle 416
 DB 1441 GGACCATGGTCGATTGTATCGACCGTTACCTGCTCTTTATT 1482

RESULT 14

US-09-058-947A-2

Sequence 2, Application US/09058947A

Patent No. 6274790

GENERAL INFORMATION:

APPLICANT: Kunst et al.
 TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
 TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klarquist Sparkman Campbell

ADDRESS: Leigh & Whinston, LLP

STREET: One World Trade Center, Suite

CITY: Portland

STATE: Oregon

COUNTRY: USA

ZIP: 97204-2988

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3.5-inch

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows NT

SOFTWARE: Word97 & ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/058,947A

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/043,831

FILING DATE: April 14, 1997

ATTORNEY/AGENT INFORMATION:

NAME: David J. Eard, Ph.D.

REGISTRATION NUMBER: 41,401

REFERENCE/DOCKET NUMBER: 5493-50032/DJE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391

TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1807

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; US-09-058-947A-2

Alignment Scores:

Pred. No.:	1,46e-136	Length:	1807
Score:	1249.50	Matches:	237
Percent Similarity:	73.43%	Conservative:	67
Best Local Similarity:	57.25%	Mismatches:	99
Query Match:	55.53%	Indels:	11
DB:	4	Gaps:	2

SEQ14-JOIN-SEQ4 (1-432) x US-09-058-947A-2 (1-1807)

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Db 323 ATCTACCTCGTGTGACTATTCTGTTACAAAGCCACCTGTCACGGTGTGCTGCCCTTCGCA 382
QY 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
Db 383 ACTTTCATGGAACACTCTCGTTTGATCCTCAAG----- 415
QY 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeuGly 62
Db 416 ---GACAAGCCTAAGACCGTCGAGTGTCCAAATGAGATCTCTTGAACGTTCTGCGCTCGGT 472
QY 63 AspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAlaAla 82
Db 473 GAGGAGACTTGTCTCCCTCGGCTATTCTATATATATCTCTCCACACCAACCTGACCGG 532
QY 83 AlaArgGluGluThrGluGlnValIleGlyAlaLeuGluAsnLeuPheLysAsnThr 102
Db 533 GCTAGACCGAGGCTCAGATGGTATCTTCGAGGCCATGAGCAGCATCTTTCAGAAACCC 592
QY 103 AsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnProThr 122
Db 593 GGTCTTAACCTAAAGACGTCGACATCTTATCGTCAACTGCTCTCTTCTCTCCACA 652
QY 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
Db 653 CCATCGCTCAGCTATGTCATCAACAATATAGCTTAGGAGTAATATCAAGAGCTTC 712
QY 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaLeuAspLeuAlaLysAspLeu 162
Db 713 AATCTTTGGGGATGGGCTGCACGCGGGCTGATCTCAGTTGATAGCCGCGACTTG 772
QY 163 LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsn 182
Db 773 CTCCCAAGTTCATCCCAATTCAATGCATCATCTGTCACGAGGAGATCATACCGCTAAT 832
QY 183 ILeTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGly 202
Db 833 TACTATCAAGGCAACGAGAGACCATGTTGTACCCAAATTGCTCTCTCCGATGGGTCG 892
QY 203 AlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuVal 222
Db 893 GCAGCCATACATATGTCACACCGCGGCTCAGCCGGTGGCGACCAATACAGCTTCC 952
QY 223 HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGly 242
Db 953 CACCTCTCGGGACACACCGCTGGCGCTGACGACAAGTCTTCTTACTGTGCTACGAAACAG 1012
QY 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
Db 1013 GAACACAAAGGACACGCTGGCATCACTTGTCCAAAGATCTCATGCCCCTCGCGGT 1072
QY 263 ArgThrValLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLys 282
Db 1073 GAAGCCCTCAAGGCAACATCACCAATAGTGTCTTGGTCTCTACCGCGCTCAGAACAA 1132

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QY 283 LeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyr 302
Db 1133 CTTCTCTTCCTCAGTCCTAATCGGACGTAAATCTTCAACCCGAATGGAACCA--- 1189
QY 303 TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAla 322
Db 1190 TACATACCGGATTCAAGCTGGCCTTCGAACACTTTTGCATTTCAGCGAGGAGGAGAGCG 1249
QY 323 ValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342
Db 1250 GTGATCGACGAGCTCAAAAGAATCTACAACATATCAGGAGAACACGTTGAGCCCTCAAGA 1309
QY 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeuAlaTyr 362
Db 1310 ATGACACTACATCGTTTGGTAACACGTCATCTTCATCTGTTATGTTAGCAGCTTAGCTAC 1369
QY 363 IleGluAlaLysGlyArgMetLysGlyAsnLysValTrpGlnIleAlaLeuGlySer 382
Db 1370 ATCAGTCTAAAGGGAGAAATGAGGAGGCGGATCGCGTTTGGCAAATCGCGTTTGGGAGT 1429
QY 383 GlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThrAsn 402
Db 1430 GGTTCAGTGTAACTCTGCCGTGTGGAATGTAAACCGTACCGTACGATTAAAGACACCTAAGGAC 1489
QY 403 SerProTrpGluHisCysIleAspArgTyrProValLysIle 416
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; RESULT 15

; US-09-058-947A-1

; Sequence 1, Application US/09058947A

; Patent No. 6274790

; GENERAL INFORMATION:

; APPLICANT: Kunst et al.

; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme

; TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klarquist Sparkman Campbell

; ADDRESSEE: Leigh & Winston, LLP

; STREET: One World Trade Center, Suite

; CITY: Portland

; STATE: OR

; COUNTRY: USA

; ZIP: 97204-2988

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disk, 3.5-inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows NT

; SOFTWARE: Word97 & ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/058,947A

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/043,831

; FILING DATE: April 14, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: David J. Earp, Ph.D.

; REGISTRATION NUMBER: 41,401

; REFERENCE/DOCKET NUMBER: 5493-50032/DJE

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 256-7391

; TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3722

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; US-09-058-947A-1

GenCore version 5.1.3
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Delop 6.0, Delext 7.0

Searched: 381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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-MAXLEN=2000000000
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Database :

Published Applications_NA.:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2234	99.3	1521	10	US-09-877-476-11	Sequence 11, Appl
6	2233	99.2	1521	10	US-09-877-476-19	Sequence 19, Appl
7	2198.5	97.7	1518	10	US-09-877-476-9	Sequence 9, Appli
8	2198.5	97.7	1524	10	US-09-877-476-3	Sequence 3, Appli
9	2191.5	97.4	1518	10	US-09-877-476-17	Sequence 17, Appl
10	2191.5	97.4	1524	10	US-09-877-476-33	Sequence 33, Appl
11	2182	97.0	1521	10	US-09-877-476-25	Sequence 25, Appl
12	2181	96.9	1521	10	US-09-877-476-39	Sequence 39, Appl
13	2161	96.0	1521	10	US-09-877-476-23	Sequence 23, Appl
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16	2143.5	95.3	1736	10	US-09-877-476-5	Sequence 5, Appli
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18	2061	91.6	1521	10	US-09-877-476-29	Sequence 29, Appl
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20	2018	89.7	1709	10	US-09-877-476-35	Sequence 35, Appl
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22	1524.5	67.8	1611	10	US-09-883-797-9	Sequence 9, Appli
23	1508.5	67.0	1548	10	US-09-883-797-13	Sequence 13, Appl
24	1492.5	66.3	1479	10	US-09-883-797-3	Sequence 3, Appli
25	1478.5	65.7	1512	10	US-09-883-797-5	Sequence 5, Appli
26	1272	56.5	1530	9	US-09-938-842A-1205	Sequence 1205, Ap
27	1249.5	55.5	1491	10	US-09-892-325-3	Sequence 3, Appli
28	1249.5	55.5	1494	9	US-09-938-842A-569	Sequence 569, App
29	1249.5	55.5	1502	10	US-09-883-797-11	Sequence 11, Appl
30	1249.5	55.5	1807	10	US-09-892-325-2	Sequence 2, Appli
31	1249.5	55.5	3722	10	US-09-892-325-1	Sequence 1, Appli
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33	1242.5	55.2	1563	9	US-09-938-842A-1552	Sequence 1552, Ap
34	1240	55.1	1587	9	US-09-938-842A-1598	Sequence 1598, Ap
35	1120	49.8	1653	9	US-09-938-842A-2597	Sequence 2597, Ap
36	1119	49.7	1650	10	US-09-883-797-7	Sequence 7, Appli
37	1059	47.1	2782	10	US-09-905-657-1	Sequence 1, Appli
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39	507	22.5	468	10	US-09-770-444-253	Sequence 253, App
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41	420	18.7	409	10	US-09-878-574-4051	Sequence 4051, Ap
42	371	16.5	387	10	US-09-878-574-1065	Sequence 1065, Ap
43	270.5	12.0	276	10	US-09-878-574-12488	Sequence 12488, A
44	216	9.6	343	10	US-09-878-574-2604	Sequence 2604, Ap
45	183.5	8.2	3114	9	US-10-037-598-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-877-476-13
; Sequence 13, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877, 476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3), having a mutation at position 275;
; NAME/KEY: CDS
; LOCATION: (1)...(1518)


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Qy 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACCTTGGTGGCATGGTGTAGTGGCGGCTTATAGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTGCATGCTCAATAAATACGATGCTCTTGGTGGACAGACAGACATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTAGCTGGTGAATAATAGTCCATGATGCTTTCAAAATGCTTCTCCGTGT 822
Qy 201 GlyGlyAlaIleLeuLeuSerAsnLysProGlyAspArgAlaGlySerLysTyrGlu 220
Db 823 GGTGGGGCGCTATTTCCTCCACAGCCCTGGAGATCGTAGCCGTCACAGTACGAG 882
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTTACACAGCTTCGAACGCATACCGAGCTGACGACAAAGTCTTTTCTGCTGCAA 942
Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGAGACGATGACAGCGCAAAATCGGAGTCAGTGTTCACAGGACATAACCGATGT 1002
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGGTCGAACGGTTTGAAGAAACATAGCAACGTTGGGTCCGCTGATCTCCGTTAAGC 1062
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
Db 1063 GAGAACTCTTTTTCGTACCTTCATCGGCGCAAGAACTTTCAAGATAAATCAAA 1122
Qy 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
Db 1123 CATTAAGTCCCGGATTTCAAACTGCTATTGACCATTTTGTATACATGCGCGAGGC 1182
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGAGCGGTGATGATGCTGACGAGAAACCTAGCCCTAGCACCGATCGATGAGGCA 1242
Qy 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrTyrGluLeu 360
Db 1243 TCAAGTCAACGCTTACATAGATTGGAAACACTTCATCTAGCTCAATGATGATGATG 1302
Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
Db 1303 GCATACATAGAAGCAAAAGGAGGATCAAGAAAGGTAATAAAGTTTGGCAGATTGCTTTA 1362
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
Db 1363 GGTGAGGCTTTAAGTGTACAGTGCAGTGTGGGTGGCTTAAACAATGTCAAGCTTCG 1422
Qy 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAAAATAGTCCTGGGAACACTGCTACGACGATACCCCGGTCAAAATGATCTGATTCA 1482
Qy 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAGTCAGACACTCGGTGTCAAAACGGTGGCTCC 1518

RESULT 4
US-09-877-476-7
; Sequence 7, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
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; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO.3); designated At114
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-7

Alignment Scores:
Pred. No.: 7,21e-264 Length: 1521
Score: 2237.00 Matches: 429
Percent Similarity: 99.54% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.42% Indels: 0
DB: 10 Gaps: 0

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-7 (1-1521)
Qy 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSer 20
Db 223 AATCGGTTTATCTGCTGACTACTCGTGTACCTTCGCCGCCGATCTCAAGTTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsn 40
Db 283 GTCTCTAAAGTCATGATATTTTACCATAATAGAAAGCTGATACTTCTTCACGGAAC 342
Qy 41 GlyThrCysAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
Db 343 GGCACGTGTGATGATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 402
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProArgLysThrPhe 80
Db 403 CTAGCCATCAAACTCACGGGCCGAGGGGTGTCAGTCTCCCTCCCGGAAGACTTTT 462
Qy 81 AlaAlaAlaArgGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCGGCGCGCGGTGAAGAGACGAGCAAGTTATCATTTGGTGCCTAGAAAATCTATTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAACGTTAACCTTAAAGATATAGTATATCTTGTGTGACTCAAGCATGTTTAA 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCATCGCTCTCCGCGATGGTTCGTTAACACTTTCAAGCTCCGAAAGCAACGTAAGA 642
Qy 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACCTTGGTGGCATGGTGTAGTGGCGGCTTATAGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTGTGATGCTCAATAAATACGATGCTCTTGGTGGACAGACAGACATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTAGCTGGTGAATAATAGTCCATGATGCTTTCAAAATGCTTCTCCGTGT 822
Qy 201 GlyGlyAlaIleLeuLeuSerAsnLysProGlyAspArgAlaGlySerLysTyrGlu 220
Db 823 GGTGGGGCGCTATTTCCTCCACAGCCCTGGAGATCGTAGCCGTCACAGTACGAG 882
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
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Db 883 CTAGTTCACAGGTTGCAACGCATACCGAGCTGACGGCAAGTCTTTTCGTTGCGTGCAG 942
Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGAGACCATGAGAACGCAAAATCGAGTGTGTTGTTCCAAAGACATAACCGATGTT 1002
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGTCGACGGTTAAGAAACATACGACGTTGGTTCGTTGATTTCTCCGTTAAGC 1062
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLys 300
Db 1063 GAGAACTTCTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAGATAAATCAAA 1122
Qy 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
Db 1123 CATTTACTAGTCCGGATTTCAAACTTCTGATTCGACATTTTGTATACATCCCGAGGC 1182
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGAGCGGTGATGATGCTAGAGAGAACCTAGCCCTAGCACCGATCGATAGAGGCA 1242
Qy 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrTyrGluLeu 360
Db 1243 TCAGATCAGCTTACATAGATTGGAACACTTCATCTAGCTCAATATGGTATGAGTIG 1302
Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
Db 1303 GCATACATAGAAACAAAGAGAGTGAAGAAAGTAATAAGTTTGGCAGATTGCTTTA 1362
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer 400
Db 1363 GGGTCAGCTTTAAGTGTACAGTGCAGTTGGTGGCTCTTAACATGTCAACGCTTCG 1422
Qy 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAATAGCTCTTGGGAACACTGCATCGACAGATACCGGTCAAAATTTGATCTGATTCA 1482
Qy 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAGTCAGAGACTCGTCCCAACGTCGGTCC 1518

RESULT 5
US-09-877-476-11
; Sequence 11, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: PARTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 342 bp from A. thaliana FAEL (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3) having mutations at positions 271, 272 and
; OTHER INFORMATION: 275; designated At114 L91C K92R
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-11

Alignment Scores: 1.68e-263 Length: 1521
Pred. No.:

Score: 2234.00 Matches: 429
Percent Similarity: 99.54% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.29% Indels: 0
DB: 10 Gaps: 0

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-11 (1-1521)

Qy 1 AspProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSer 20
Db 223 AATCCCGGTTTATCTCGTTGACTACTCGTTTACCTTCCGCCACCGCATTTGAGAGTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db 283 GTCTCTAAAGTCATGATATTTCTACCAATAAAGAAAGCTGATACTTCTTCACGGAAC 342
Qy 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
Db 343 GGCACGTGTGATAAATTCGTCTGCTTGGCTTCTTGGAGGAAGATTCAAGAACTTCAGGT 402
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGCGCATGAACTCACGGCCCGAGGGCTGCTTCAGTCCCTCCCGGAAGACTTTT 462
Qy 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 CGGGCGCGCGCTGAAGAGACGAGCAAGTTATCATTTGGTGGCTAGAAAAATCTATTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 ACACCAACGTTAACTTAAGATATAGGTATACTTGTGGTGAACCTCAAGCATGTTTAA 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCATCTCGCGCATGCTGTTAAACACTTCAAGCTCCGGAAGCAAGTAAAGA 642
Qy 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACTTGGTGGCATGGTGTAGTCCGCGCTTATAGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTGTCATGTCATATAAATACGTATGCTTGTGGTGAGCAGACAGAACTCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAAATGCTTGTCCGTGTT 822
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGCGCGCTATTTGCTCTCCAAACGCTGGAGATCGTAGACGGTCCCAAGTACGAG 882
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTACACGCTTCCGAACGATACCGAGCTGACGGCAAGTCTTTTCGTTGCGTCAA 942
Qy 241 GluGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGAGACATGAGACGCAAAATCGAGTGTGTTGTCGAAGACATACCGCATGTT 1002
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGTCGCAACGGTTAAGAAAAACATACCAACGTTGGTTCGTTGATTTCTCCGTTAAGC 1062
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLys 300
Db 1063 GAGAACTTCTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAGATAAATCAAA 1122
Qy 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
Db 1123 CATTTACTAGTCCCGGATTTCAAACTTCTGATTCGACATTTTGTATACATCCCGAGGC 1182
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340

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Db 1183 AGAGCGTGATGATGCTAGAGAGAACTAGCCCTAGCACCGATCGATGAGGCA 1242
Qy 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTrpTyrGluLeu 360
Db 1243 TCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGATGATGTTG 1302
Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTTPGlnIleAlaLeu 380
Db 1303 GCATACATAGAACAAAGGAGGATGAGAAAGGTATTAAGTTTGGCAGATGCTTTA 1362
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTTPValAlaLeuAsnAsnValLysAlaSer 400
Db 1363 GGGTCAGGCTTAAAGTGTAAAGTGCAGTTTGGTGGCTCTAAACAATGCAAGCTTGG 1422
Qy 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAATAGTCCCTTGGGAACACTGCATCGACAGATACCCGGTCAAAATGATCTGATTCA 1482
Qy 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAGTCAGAGACTCGTGTCCCAAAACGGTCGGTCC 1518

RESULT 6
US-09-877-476-19
; Sequence 19, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 342 bp from A. thaliana PAE1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3) having mutations at positions 271, 272, 275
; OTHER INFORMATION: and 920; designated At14 L91C K92R G307D;
; OTHER INFORMATION: hypothetical
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-19

Alignment Scores:
Pred. No.: 2,236-263 Length: 1521
Score: 2233.00 Matches: 429
Percent Similarity: 99.54% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.24% Indels: 0
DB: 10 Gaps: 0

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-19 (1-1521)
Qy 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSer 20
Db 223 AATCCGGTTTATCTCGTTGACTACTCGTTTACCTTCGCCACCGCATTCGACAGTTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db 283 GTCTTAAGTCATGGNATTTTCTACCAAAATAGAAAAGCTGATCTTTCACGGAC 342
Qy 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
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Db 343 GCCACGTGTGATAAATTCGTCGTGGCTTGCATCTTCTGAGGAAGATTCAAGACGTTTCAGGT 402
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGCGCATGAAACTCACGGGCCGAGGGGCTGCTTCAGGTCTCCCGGAAGACTTTT 462
Qy 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 CGGGGGCGGCTGAAGAGACGGGAAGTTATCATTTGGTCGCTGAAAATCTATTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAACGTTAACCTTAAGATATAGGTATATCTTGTGCTGAACCAAGCATGTTTAA 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCACTCCATCGCTTCCCGGATGGTGTAACTTTCAGCTCCGAAGCAACGTAAGA 642
Qy 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACCTTGGTGGCATGGTGTAGTCCCGCGCTTATAGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTTCATGTCCTCAAAAATACGTATCTCTTGTGTGAGACAGAGAACATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTTACGCTGGTGATTAATAGTCCCATGATGTTTCAAAATGCTTTCGCTGT 822
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGCGCTATTGCTCTCCAAACAAAGCTGGAGTCTAGACGGTCCAAAGTACGAG 882
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTCCACACGGTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTTGCGTCAA 942
Qy 241 GinglyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGAGACGATGAGAAACGCAAAATCGAGTGTGTTGCCAAGGACATACCCGATGTT 1002
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuProLeuSer 280
Db 1003 GCTGGTCCGACGGTTTAAAGAAAACATAGCAACGTGGGTCCGCTGATTTCCCGTTAAGC 1062
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
Db 1063 GAGAAACTTCTTTTTCGTTACCTTCATGGGCAAGAAACTTTTCAAAAGATAAAATCAA 1122
Qy 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyCly 320
Db 1123 CATTTACTAGTCCCGGATTTCAAACTTGTATTGACCATTTTGTATATACATGCCGGAGGC 1182
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGAGCCGTGATGATGCTGCTAGAGAAACCTAGCCCTAGCACCGATCGATGAGGCA 1242
Qy 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTrpTyrGluLeu 360
Db 1243 TCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGATGATGATG 1302
Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTTPGlnIleAlaLeu 380
Db 1303 GCATACATAGAACAAAGGAGGATGAGAAAGGTATTAAGTTTGGCAGATGCTTTA 1362
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTTPValAlaLeuAsnAsnValLysAlaSer 400
Db 1363 GGGTCAGGCTTAAAGTGTAAAGTGCAGTTCAGTTGGTGGCTCTAAACAATGTCAGGCTTCG 1422
Qy 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAATAGTCCCTTGGGAACACTGCATCGACAGATACCCGGTCAAAATGATCTGATTCA 1482
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QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
 |||
 Db 1483 GGTAAGTCAGACACTCGTGTCCAAAACGGTCGGTCC 1518

RESULT 7

US-09-877-476-9
 ; Sequence 9, Application US/09877476
 ; Patent No. US20020049994A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Blacklock, Brenda J.
 ; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
 ; FILE OF INVENTION: SYNTHASE POLYPEPTIDES
 ; FILE REFERENCE: 07148-108001
 ; CURRENT APPLICATION NUMBER: US/09/877,476
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,326
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 1518
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 ; OTHER INFORMATION: 3' 1296 bp from B. napus elongase KCS (SEQ ID
 ; OTHER INFORMATION: NO.3); designated AT4
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1515)
 US-09-877-476-9

Alignment Scores:
 Pred. No.: 3,7e-259 Length: 1518
 Score: 2198.50 Matches: 423
 Percent Similarity: 98.84% Conservative: 3
 Best Local Similarity: 98.14% Mismatches: 4
 Query Match: 97.71% Indels: 1
 DB: 10 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-9 (1-1518)

QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
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 Db 226 CCGGTTTACCTCGTGTAGTACTCATGCTACCTCCACCACGATGTAGATCAAGTATC 285
 QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41
 |||
 Db 286 TCCAAAGGTCATGGATATCTTTATCAAGTAAAGAAAGCTGAT---CCTTCTCGGAACGGC 342
 QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
 |||
 Db 343 ACGTCCGATGACTCGTGGTGTGACITCTTGAGGAGATTCAGAACGTTTCAGGTCTA 402
 QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
 |||
 Db 403 GCGCATGAATCAACGGCCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTGGC 462
 QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
 |||
 Db 463 GCGGCGGTGAAGAGAGGAGCAAGTATCATTTGTCGCTAGAAATCTATTCAGAAC 522
 QY 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
 |||
 Db 523 ACCAACGTTAACCCCTAAAGATAGGTATCTTGTGTGAACCTCAAGCATGTTTAAATCCA 582
 QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
 |||
 Db 583 ACTCCATCGTCTCCGGATGTCGTTAACACTTCAAGTCCGAGCAACCTAGAACG 642
 QY 142 PheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaLeuAspLeuAlaLysAsp 161
 |||

Db 643 TTTAACCTTGGTGGCATGGTTGTAGTCCGGCGCTTATAGCCATTGATCTAGCAAGGAC 702
 QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
 |||
 Db 703 TTGTTCATGTCCATAAAAAATACGTATGCTCTTGTGTGGTGGACACAGAACATCATTAT 762
 QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 |||
 Db 763 AACATTTACCTCGTGTATAGTATAGTTCATGATGTTTCAAAATGCTTGTTCGGTGTGGT 822
 QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
 |||
 Db 823 GGGCGCGCTATTTTGTCTCTCCAAACAGCCTGGAGATCGTAGACGGTCCCAAGTACGAGCTA 882
 QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
 |||
 Db 883 GTTCACACGGTTCGAACGATACCGAGCTGACGGCAAGTCCTTTTCGTTGGTGGCAACA 942
 QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
 |||
 Db 943 GGAGACGATGAGAACGGCAAAATCGGAGTGTGTCTCCAAAGACATAACCGATCTTGCT 1002
 QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
 |||
 Db 1003 GGTGCAACGGTTAAGAAAACATACGACGTTGGTCCGTGTGATCTTCCGTTAAGCGAG 1062
 QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
 |||
 Db 1063 AAACCTCTTTTTCGTTACCTTTCATGCGGCAAGAACTTTTCAAAAGATAAAATCAACAT 1122
 QY 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
 |||
 Db 1123 TACTACGTCGGGATTCAAACTGCTATTGACCATTTTGTATACATGCCGGAGGAGAGA 1182
 QY 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
 |||
 Db 1183 GCGGTGATGATGTGCTAGAGAAGAACCTAGCCCTAGCAGCATCGATGATGAGGATCA 1242
 QY 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeuAla 361
 |||
 Db 1243 AGATCAACGTTACATAGATTTGGAAACACTTCATCTAGTCAATATGTTATGATGTTGGCA 1302
 QY 362 TyrIleGluAlaIleGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
 |||
 Db 1303 TACATAGAACGAAAAGGAGGATGAAGAAAGGTAATAAAGTTTGGCAGATTGCTTTAGGG 1362
 QY 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr 401
 |||
 Db 1363 TCAGGCTTTAAGTGTAAACAGTGCAGTTTGGTGGCTCTAAACAATGTCNAAGCTTCGACA 1422
 QY 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
 |||
 Db 1423 AATAGTCCCTGGGAACACTGTCATGACAGATACCCGGTCAAAATTCATTCGATTCAGGT 1482
 QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
 |||
 Db 1483 AAGTCAGAGACTCGTGTCCAAAACGGTCCGTCC 1515

RESULT 8

US-09-877-476-3
 ; Sequence 3, Application US/09877476
 ; Patent No. US20020049994A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Blacklock, Brenda J.
 ; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
 ; FILE OF INVENTION: SYNTHASE POLYPEPTIDES
 ; FILE REFERENCE: 07148-108001
 ; CURRENT APPLICATION NUMBER: US/09/877,476
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,326
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1524

TYPE: DNA

ORGANISM: Brassica napus

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1521)

US-09-877-476-3

Alignment Scores:

Pred. No.: 3,73e-259 Length: 1524

Score: 2198.50 Matches: 423

Percent Similarity: 98.84% Conservative: 3

Best Local Similarity: 98.14% Mismatches: 4

Query Match: 97.71% Indels: 1

DB: 10 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-3 (1-1524)

```
Qy 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
Db 229 CCGGTTTACCTCGTTGACTCATCTGCTACCTTCCACCAACGCAATGTGATCAAGTATC 288
Qy 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
Db 289 TCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAGCTGAT---CCCTCTCGGAACGGC 345
Qy 42 ThrCysAspAspSerSerTyrLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
Db 346 ACGTGCAGTACTCGTCTGCTGCTTACTTCTTGAGGAAGATTCAGGAAGCTTCAGGTCCTA 405
Qy 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
Db 406 GGGGATGAACACTCAGCGGCCGAGGGGCTGCTTCAGGTCCTCCCGGAAGACTTTTGGC 465
Qy 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
Db 466 CGCGCGCTGAAGACGAGCAAGATTATCATTTGGTGGCTAGAGAAATCTATTCAAGAAC 525
Qy 102 ThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnPro 121
Db 526 ACCAAGTTAACCTTAAGATATAGGTATCTTGTGTGACTCAGCATTTTATATCCA 585
Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
Db 586 ACTCCATCGCTCTCGCGCATGGTCTGTTAACACTTTCAAGCTCCGAAGCAACGTAAGAAGC 645
Qy 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db 646 TTTTAACCTTGGTGGCATGGTGTGATGCGCGGCTTATAGCCATTTGATCTAGCAAGGAC 705
Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
Db 706 TTGTGTCATGTCATAAAAATACGTATGCTCTTGTGTGAGCAGACAGAAACATCACTTAT 765
Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
Db 766 AACATTAGCGTGGTGATATAAGTCCATGATGTTTCAAAATGCTTCTCCGTTGGT 825
Qy 202 GlyAlaAlaIleLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 826 GGGCGCGCTATTTTGTCTCCCAACAGCCCTGGAGATCGTAGAGGTCCTCAAGTACGAGCTA 885
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 886 GTTCACACGGTTCGACCGCATACCGAGCTGAGCGCAAGTCTTTTCGTTGGTGCACAA 945
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db 946 GGAGACCATCAGAACGGCAAAATCGAGTGGTGTTCCTCAAGGACATAACCGATGTGCT 1005
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
```

```
Db 1006 GGTGGAACGGTTAAGAAAAACATAGAACGGTGGGTCGGTTCCTCCGTAAAGCGAG 1065
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLysHis 301
Db 1066 AAACCTTCTTTTTCGTTACCTTCATGCGGCAAGAACTTTTCAAGATAAATCAACAT 1125
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArg 321
Db 1126 TACTACGTCGCGGATTCAAACTTGTATGACCATTTTGTATACATCCGAGGCGACA 1185
Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db 1186 GCGGTGATTGATGTGTAGAGAAGAACCTAGCCCTAGCAGCATCGATGTAGAGGCATCA 1245
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleThrPyrGluLeuAla 361
Db 1246 AGATCAACGTTTACATAGATTTGGAACACTTCTATCTAGCTCAATATGGTATGAGTTGGCA 1305
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
Db 1306 TACATAGAAGCAAAAGAGGATGAAGAAAGTAATAAAGTTTGGCAGATTGCTTTAGGG 1365
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401
Db 1366 TCAGGCTTTAAGTGTACACAGTGTGGGTGGCTCTAACCAATGTCAAGCTTCGACA 1425
Qy 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysLysLysAspSerGly 421
Db 1426 AATAGTCTCTGGGAACACTGTCATCGACAGATACCGGTCGCAAAATTTGATCTGATTCAGT 1485
Qy 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1486 AAGTCAGAGACTCGTGTCCAAACGGTCGGTCC 1518
```

RESULT 9

US-09-877-476-17

Sequence 17, Application US/09877476

Patent No. US20020049994A1

GENERAL INFORMATION:

APPLICANT: Jaworski, Jan G.

APPLICANT: Blacklock, Brenda J.

TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

FILE REFERENCE: 07148-108001

CURRENT APPLICATION NUMBER: US/09/877,476

CURRENT FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/210,326

PRIOR FILING DATE: 2000-06-08

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17

LENGTH: 1518

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: 5' 222 bp from A. thaliana PAEL (SEQ ID NO:1) and

OTHER INFORMATION: 3' 1296 bp from B. napus elongase KCS (SEQ ID

OTHER INFORMATION: NO:3) having a mutation at position 917;

NAME/KEY: CDS

LOCATION: (1)...(1515)

US-09-877-476-17

Alignment Scores:

Pred. No.: 2,66e-258 Length: 1518

Score: 2191.50 Matches: 422

Percent Similarity: 98.61% Conservative: 3

Best Local Similarity: 97.91% Mismatches: 5

Query Match: 97.40% Indels: 1

DB: 10 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-17 (1-1518)

QY	102	Thr	Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	Phe	Asn	Pro	121
Db	526	ACC	AA	CGT	TAA	CCT	AAA	GAT	AT	AGT	TAT	ACT	TGT	GGT	GAA	CTC	AA	CTC	AA	AGT	CTT	585
QY	122	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu	Arg	Ser	Asn	Val	Arg	Ser	141
Db	586	ACT	CC	ATC	CTC	CTC	CGG	GAT	GGT	CGT	TAA	CAC	TTT	CA	AGC	TTC	CG	GA	AGC	CA	AGT	645
QY	142	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	161
Db	646	TTT	AA	CC	T	TGG	TGC	AT	GGG	TGT	TAG	TCC	CGG	CGT	TAT	AGC	CAT	T	GAT	C	T	705
QY	162	Leu	Leu	His	Val	His	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	181
Db	706	TTG	TT	GC	AT	GC	TAT	AAA	AAA	TAC	GAT	GCT	TCT	TG	TG	TG	G	AGC	AG	CA	CAT	765
QY	182	Asn	Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	I	Ser	Asn	Cys	Leu	Phe	Arg	Val	201
Db	766	AAC	AT	TTA	ACG	TGG	TGAT	ATAT	AGG	TCC	ATG	ATG	GGT	TTT	CA	AA	T	GCT	GT	T	GGT	825
QY	202	Gly	Ala	Ala	Ile	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg	Ser	Lys	Tyr	Glu	Leu			221
Db	826	GGG	CG	CGC	TAT	TTT	GC	TCT	CCA	CA	AGC	CTG	CAG	AT	CGT	AG	CGG	TCC	AA	G	T	885
QY	222	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	241
Db	886	GTT	CA	ACG	GGT	TCG	AGC	ATC	CGG	AGT	GAC	CA	AGT	CTT	TTC	TG	TG	TG	CGT	GC	AC	945
QY	242	Gly	Asp	Asp	Glu	Asn	Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	261
Db	946	GG	AG	ACG	AT	GAG	AGC	CA	AAA	AT	CGG	ATG	TGG	ATG	TCC	AA	G	AGC	ATA	AC	CG	1005
QY	262	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr</											

```

; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO. 25
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1002 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3); designated At173
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-25

Alignment Scores:
Pred. No.: 3 88e-257 Length: 1521
Score: 2182.00 Matches: 420
Percent Similarity: 98.36% Conservative: 5
Best Local Similarity: 97.22% Mismatches: 0
Query Match: 96.98% Indels: 0
DB: 10 Gaps: 0

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-25 (1-1521)

```



```
Db 1063 GAGAAACTTCTTTTTCGTTTACCTTCATGGGCAAGAACTTTTCAAGATAAAATCAAA 1122
Qy 301 HlSTyTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHlSAlaGlyGly 320
Db 1123 CATTTACTAGCTCCGGATTTCAAACTTGCTATTGACCATTTTGTATATACATCCGGAGGC 1182
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGAGCCGCTGATGATGCTAGAGAGAACTAGCCCTAGCACCGATCGATGAGAGGCA 1242
Qy 341 SerArgSerThrLeuHlSArgPheGlyAsnThrSerSerSerSerIleTyrGluLeu 360
Db 1243 TCAAGATCAACGCTTACATAGATTTGGAAACACTTTCATCTAGCTCAATATGATGATGTTG 1302
Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
Db 1303 GCATACATAGAGAAAGGAAGGATGAAGAAAGGTAATAAGTTTGGCAGATTGCTTTA 1362
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
Db 1363 GGGTCAGGCTTTAAGTGTAAAGTGCAGTTTGGGTGGCTTAAACAATGTCAAAAGCTTCG 1422
Qy 401 ThrAsnSerProTrpGluHlSArgPheGlyAsnLysValTrpValLysIleAspSerAspSer 420
Db 1423 ACAATAGTCCCTGGGAACACTGCTGCAGATACCCGGTCANAAATTGATTCGTATCA 1482
Qy 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAGTCAGAGACTCGTGTCCAAAACGGTCCGGTCC 1518
```

RESULT 13

```
US-09-877-476-23
; Sequence 23, Application US/09877476
; Patent No. US2002004994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 759 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3); designated At254
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-23
```

```
Alignment Scores:
Pred. No.: 1,44e-254 Length: 1521
Score: 2161.00 Matches: 414
Percent Similarity: 98.15% Conservative: 10
Best Local Similarity: 95.83% Mismatches: 8
Query Match: 96.04% Indels: 0
DB: 10 Gaps: 0
```

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-23 (1-1521)

```
Qy 1 AsnProValTyrIleuValAspTyrSerCysTyrIleuProProHlSLeuArgValSer 20
Db 223 AATCCGGTTTATCTCGTTGACTACTCGTGTACTTTCCACCACCGCATCTCAAAAGTTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
```

```
Db 283 GTCTCTAAAGTCATGATATTTTACCAATAAGAAAGCTGATACTTCTTTCACGGAAAC 342
Qy 41 GlyThrCysAspAspSerSerTyrIleuAspPheLeuArgLysIleGlnGluArgSerGly 60
Db 343 GTGGCATGTGATGATCCGCTCCTCGCTCGATTTCTCTGAGGAAGATTCAAGAGCGTTACAGT 402
Qy 61 LeuGlyAspGluThrHlSgLyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGGTGATGAGACGCTACAGTCTCTGAGGAGCTATTCCATACACCGCGGAAGACTTTT 462
Qy 81 AlaAlaLargGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCAGCGTCACGTGAAGACAGACAGAGAGGTTCATCGTGCCTCGCTCGAAATCTATTTCGAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAAGTTTAACCTTAGAGAGATTGGTATCTTGTGTGAACCTCAAGCATGTTTAAAT 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCTTCGCTATCCGCTATGCTGTTAATACTTTCAAGCTCCGAAGCAACATCAA 642
Qy 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAATCTAGAGAGATGGGTGTAGTGTGTGTATTGTCATTTGATTTGCTTAA 702
Qy 161 AspLeuLeuHlSValHlSAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTGTCATTTCAATAAAACACTTATGCTCTCGTGTGAGCACAGAACATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGGTGTATATAGTCCATGATGGTTTCAAAATGCTTGTTCGCTGT 822
Qy 201 GlyGlyAlaLalLeuLeuSerAsnLysProGlyAspArgArgArgSerLysTyrGlu 220
Db 823 GGTGGGCGCGTATTTGCTCTCCAAAGCCTGGAGATCGTAGACGGTCCCAAGTACGAG 882
Qy 221 LeuValHlSThrValArgThrHlSThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTTCACGGTTCGACGCATACCGGAGCTGACGCAAGTCTTTTCGTTGCGTGCA 942
Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGAGACGATGAGAACGGCAAAATCCGAGTGAAGTTTGTCCAAGGACATAACCGATGT 1002
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGCTCAACGGTTAGAAAACATAGCAAGTTGGTCCGTTGATTTCTTCGTTNAGC 1062
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLysLeuPheLysAspLysLys 300
Db 1063 GAGAAACTCTTTTTTTCGTTTACCTTCATGGGCAAGAACTTTTCAAGATAAATCAAA 1122
Qy 301 HlSTyTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHlSAlaGlyGly 320
Db 1123 CATTTACTAGCTCCGGATTTCAAACTTGCTATTGACCATTTTGTATACATCCGGAGGC 1182
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGAGCCGCTGATGATGCTAGAGAGAACTAGCCCTAGCACCGATCGATGAGAGGCA 1242
Qy 341 SerArgSerThrLeuHlSArgPheGlyAsnThrSerSerSerSerIleTyrGluLeu 360
Db 1243 TCAAGATCAACGCTTACATAGATTTGGAAACACTTTCATCTAGCTCAATATGATGATGTTG 1302
Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
Db 1303 GCATACATAGAGAAAGGAAGGATGAAGAAAGGTAATAAGTTTGGCAGATTGCTTTA 1362
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
```



```
Db 1363 GGGTCAGGCTTTAAAGTGTAAACAGTCAGTTTGGGTGGCTTAACAAATGTCAAAGCTTCG 1422
QY 401 ThrAsnSerProTrrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAATAGTCTCTGGGAACACTGCATCGACAGATACCCGGTCAAAATGATTCTGATTCA 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAGTCAGAGACTCGTGTCCCAACACGGTCGGTCC 1518
RESULT 14
US-09-877-476-37
; Sequence 37, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 762 bp from A. thaliana FAEL (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 759 bp from B. napus elongase KCS (SEQ ID NO:3)
; OTHER INFORMATION: and having a mutation at position 920; designated
; OTHER INFORMATION: At254 G307D; hypothetical
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-37
Alignment Scores:
Pred. No.: 1.91e-254 Length: 1521
Score: 2160.00 Matches: 414
Percent Similarity: 98.15% Conservative: 10
Best Local Similarity: 95.83% Mismatches: 8
Query Match: 96.00% Indels: 0
DB: 10 Gaps: 0
SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-37 (1-1521)
QY 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSer 20
Db 223 AATCGGTTTATCTCGTTGACTACTCGTTTACCTTCCACCACCGCATCTCAAGTTAGT 282
QY 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsn 40
Db 283 GTCTCTAAAGTCATGGGATATTTCTACCAATAAAGAAAGTATCTCTTCACGGGAC 342
QY 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
Db 343 GTGGCATGTGATGATCGCTCGTTCGATTTCCTGAGGAAGATTCAAGAGCGTTTCAGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGGTGATGAGAGCTTACAGTCTCTGAGGAGCTCATCTCAGTACCCACCGGGAAGACTTTT 462
QY 81 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCAGCGTCACGTGAAGAGACAGAGAAGGTTATCATCGTGGCTCGGCTCGAAAAATCTATTCCGAG 522
QY 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAAGTTACCTCTAGAGAGATTGGTACTTGTGTGTAAGTCAAGACATGTTTAAAT 582
```

```
QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCCTTCGGTATATCCCGCTATGCTGTTAATATCTTCAAGCTCCGAAGCAATCAAA 642
QY 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAATCTAGSAGAAATGGTTGTAGTCTGGTGTATTGCTCATTTGATTTGGCTTAA 702
QY 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTTCATGTTTCATAAAACACTTATGCTCTCGTGTGAGACACAGACAATCACT 762
QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGTGATATAATAGTCCCATGATGGTTTCAAAATGCTTGTTCGGTGT 822
QY 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGCGCGCTATTTTGTCTTCCCAACAGCTGGAGATCGTAGACGGTCCCAAGTACGAG 882
QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
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QY 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
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QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
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QY 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
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QY 301 HistTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
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QY 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTrpGluLeu 360
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QY 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
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QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAGTCAGAGACTCGTGTCCCAACACGGTCGGTCC 1518
RESULT 15
US-09-877-476-31
; Sequence 31, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
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; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 1197 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3) and 3' 324 bp from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:1); designated Bn399
; NAME/KEY: CDS
; LOCATION: (1)...(1519)
; US-09-877-476-31

Alignment Scores:
Pred. No.:      8,59e-253      Length:      1521
Score:          2146.50        Matches:      412
Percent Similarity: 96.98%      Conservative: 6
Best Local Similarity: 95.59%      Mismatches: 12
Query Match:      95.40%      Indels:      1
DB:              10          Gaps:         1

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-31 (1-1521)
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Qy  22  SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
Db  289  TCCAAGGTCATCGATATCTTTTATCAAGTAAGAAAGAGCTGAT---CCTTCTCGGAACGGC 345
Qy  42  ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
Db  346  ACGTGCAGTACTCGCTGCTGGCTTGACTTCTTGAGGAGAGATTCAAGAACGTTTCAGGTCTA 405
Qy  62  GlyAspGluThrHisGlyProGluGlyLeuGlnValProToArgLysThrPheAla 81
Db  406  GGGGATGAACACTCAGCGGCCGAGGGGCTGCTTCAGGTCCTCCCGGGAAGACTTTTGGC 465
Qy  82  AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
Db  466  CGCGCGCTGAAGAGACGAGCAAGTTATCATTTGGTGGCTAGAAAAATCTATTCAAGAAC 525
Qy  102  ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
Db  526  ACCAAGCTTAAACCCATAAGATATAGGTATAGTGTGCTGAGTCAAGCATGTTTATATCCA 585
Qy  122  ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
Db  586  ACTCCATCGCTCTCCGCGATGGTGGTTAACACTTTCAAGCTCCGAAGCAACGTAAGAAGC 645
Qy  142  PheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db  646  TTTAACTTGGTGGGATGGGTGTAGTGGCGGCTTATAGCCATTTGATCTAGCAAGGAC 705
Qy  162  LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
Db  706  TTGTTGCATGTCATAAAAATACGTATGCTTTGTGGTGAGCACAGAGAACATCACTTAT 765
Qy  182  AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnProCysLeuPheArgValGly 201
Db  766  AACATTTACGCTGGTGTGATATAGTTCATGATGTTTCAAAATGCTTGTCCCGTGGT 825
Qy  202  GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
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Qy  222  ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
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Qy  242  GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db  946  GGAGACCATCAGAACGCAAAATCGGAGTGTGTTGTCGAAGGACATAACCGATGTTGCT 1005
Qy  262  GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSerGlu 281
Db  1006  GGTGCAACGGTTAAGAAAAACATACGACGTTGGTCCGTTGATTCTCCGTTAAGCGAG 1065
Qy  282  LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
Db  1066  AAACCTCTTTTTCGTTACCTTCATGGCAAGAAACTTTTCAAGATATAAATCAACAT 1125
Qy  302  TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
Db  1126  TACTACGTCCCGGATTTCAAACTTCTATTGACCATTTTGTATACATCCCGAGGCGAGA 1185
Qy  322  AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db  1186  GCCGTGATCGATGAGCTAGAGAAACCTTAGGACTATCCGCGATCGATGCGAGGCATCT 1245
Qy  342  ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleThrPyrGluLeuAla 361
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Db  1306  TACATAGAGCAAGGGAAGAAATGAAGAAAGGAATAAAGCTTTGGCAGATTGCTTTAGGA 1365
Qy  382  SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401
Db  1366  TCAGGGTTTAAAGTGTAAATAGTCGGGTTTGGGTGGCTCTACGCAATGTCAAGCATCGGCA 1425
Qy  402  AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
Db  1426  AATAGTCCTTGGCAACATTGCATCGATAGATATCCGGTAAATAATGATTCTGATTGTCA 1485
Qy  422  LysSerGluThrArgValGlnAsnGlyArgSer 432
Db  1486  AAGTCAAAAGACTCATGTCTCCAAAACGGTCGGTCC 1518
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Search completed: January 6, 2003, 20:28:29

Job time : 74.5 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2003, 14:56:55 ; Search time 187 Seconds
(without alignments)
5202.477 Million cell updates/sec

Title: SEQ14-JOIN-SEQ4

Perfect score: 2250

Sequence: 1 NPVLVDVSCYLPPLPHLRVS.....PVKIDSDSGKSETRVQNGRS 432

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=N_Geneseq_101002 -QFWT=fastp -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-USER=MCEFWA09877476 -CGEN_1.1.218 -runat_06012003.124916.9 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2244	99.7	1521	24	AAD28506	A. thaliana FAEL-B
2	2243	99.7	1521	24	AAD28510	A. thaliana FAEL-B
3	2241	99.6	1521	24	AAD28503	A. thaliana FAEL-B
4	2240	99.6	1521	24	AAD28507	A. thaliana FAEL-B
5	2237	99.4	1521	24	AAD28535	Alternative versio
6	2234	99.3	1521	24	AAD28505	A. thaliana FAEL-B
7	2233	99.2	1521	24	AAD28509	A. thaliana FAEL-B
8	2198.5	97.7	1518	24	AAD28504	A. thaliana FAEL-B
9	2198.5	97.7	1524	24	AAD28501	Brassica napus fat
10	2191.5	97.4	1518	24	AAD28508	A. thaliana FAEL-B
11	2191.5	97.4	1524	24	AAD28516	Brassica napus fat
12	2191.5	97.4	1588	22	AAF62738	Plant FAEL gene 5'
13	2191.5	97.4	1785	22	AAF61744	B. napus KCS cDNA
14	2191.5	97.4	1785	22	AAF61746	B. napus KCS cDNA
15	2191.5	97.4	1790	22	AAF62741	Brassica napus FAE
16	2188	97.2	1521	24	AAD28512	A. thaliana FAEL-B
17	2182	97.0	1521	24	AAD28536	Alternative versio
18	2181	96.9	1521	24	AAD28519	A. thaliana FAEL-B
19	2161	96.0	1521	24	AAD28511	A. thaliana FAEL-B
20	2160	96.0	1521	24	AAD28518	A. thaliana FAEL-B
21	2146.5	95.4	1521	24	AAD28515	Brassica napus fat
22	2143.5	95.3	1736	24	AAD28502	Brassica napus fat
23	2139.5	95.1	1521	24	AAD28520	B. napus elongase
24	2067	91.9	1521	24	AAD28514	A. thaliana FAEL-B
25	2061	91.6	1521	24	AAD28537	Alternative versio
26	2029.5	90.2	1521	24	AAD28513	Brassica napus fat
27	2018	89.7	1709	24	AAD28517	Arabidopsis thalia
28	2015	89.6	1641	17	AAT27036	Arabidopsis thalia
29	2015	89.6	1709	24	AAD28500	Arabidopsis fatty
30	2015	89.6	1792	21	AA235524	Fatty acid elongas
31	2014.5	89.5	1442	16	AAQ90212	Brassica Reston va
32	1985.5	88.2	1442	16	AAQ90211	Brassica condensin
33	1862.5	82.8	1664	16	AAQ90218	Condensing enzyme
34	1654	73.5	4313	24	AA72086	DNA sequence of Lf
35	1524.5	67.8	1511	20	AA723221	A. thaliana EL5 DN
36	1524.5	67.8	1853	21	AAQ50224	Arabidopsis thalia
37	1508.5	67.0	1548	20	AAQ32223	A. thaliana EL7 DN
38	1497.5	66.6	1855	21	AAQ37776	Arabidopsis thalia
39	1492.5	66.3	1479	20	AAQ32318	A. thaliana EL2 DN
40	1484	66.0	1464	21	AAQ42778	Arabidopsis thalia
41	1484	66.0	2509	22	AAQ62693	Arabidopsis KCS2 q
42	1478.5	65.7	1512	20	AAQ32319	A. thaliana EL3 DN
43	1470	65.3	1819	21	AAQ39559	Arabidopsis thalia
44	1466	65.2	1704	16	AAQ30217	Condensing enzyme
45	1377.5	61.2	2143	22	AAH50968	Ketoacyl ACP synth

ALIGNMENTS

RESULT 1

AAD28506

ID AAD28506 standard; DNA; 1521 BP.

AC AAD28506;

XX

DT 22-APR-2002 (first entry)

DE A. thaliana FAEL-B. napus elongase KCS chimeric gene, At114 mutant #2.

KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;

XX very long chain fatty acid; VLCFA; FAEL gene; chimeric; mutant; ds.

OS Chimeric - Arabidopsis thaliana.

XX Chimeric - Brassica napus.

PH Key Location/Qualifiers

FT CDS 1..1521

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FT      replace (275, A)
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FT      /*tag= d
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XX      13-DEC-2001.
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XX      08-JUN-2001; 2001WO-US18737.
XX
XX      08-JUN-2000; 2000US-210326P.
XX      (UYMI-) UNIV MIAMI.
XX
XX      Jaworski JG, Blacklock BJ;
XX
XX      WPI: 2002-154572/20.
XX      P-PSDB; AEL1614.
XX
XX      New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
XX      acids encoding the polypeptide, useful for producing very long chain
XX      fatty acids
XX
XX      Disclosure: Fig 2-7; 139pp; English.
XX
XX      The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
XX      (KCS) polypeptides with altered substrate specificity and/or catalytic
XX      activity and nucleic acid molecules encoding such polypeptides.
XX      Polypeptides of the invention are useful for catalysing the condensation
XX      of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
XX      of C20 fatty acyl CoA. They are especially useful for producing very
XX      long chain fatty acids (VLCFA) and may be used in the development of
XX      reagents for various purposes, e.g., immunological reagents to monitor
XX      expression of elongase KCS polypeptides or nucleic acid probes or
XX      primers to monitor inheritance of an elongase KCS gene in plant breeding
XX      programs. The present sequence is a mutant of Arabidopsis thaliana FAEL-
XX      Brassica napus elongase KCS chimeric gene, At114 designated as
XX      At114 K92R.
XX
XX      Sequence 1521 BP; 412 A; 342 C; 344 G; 423 T; 0 other;

Alignment Scores:
Pred. No.:      6,13e-235      Length:      1521
Score:          2244.00      Matches:      431
Percent Similarity: 99.77%      Conservative: 0
Best Local Similarity: 99.77%      Mismatches: 1
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SEQ14-JOIN-SEQ4 (1-432) x AAD28506 (1-1521)

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Db      |||||||
QY      223 AATCGGTTATCTCGTGACTACTCGTGTTACCTTCCGCCCAACCGCATCTCAGAGTTAGT 282
Db      |||||||
QY      21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db      |||||||
QY      41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnArgSerGly 60
Db      |||||||
QY      343 GCCACGTGTCATGATCGTGGCTGCACCTCTTCCAGGAATTCAGACGTTACAGT 402
Db      |||||||
QY      61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db      |||||||

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Db      403 CTAGGCGATGAACCTCACGGGCCCGAGGGGCTGCTTCAGGTCCTCCCGGAGAACTTTT 462
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Db      463 GCGGCGCGCGTGAAGAGACGGCAAGTTATCATTTGGTGGCTAGAAATATTAATTCAG 522
QY      101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db      523 AACACCAACGTTAACCTTAAGCATATAGGTATCTTGGTGAACCAAGCATGTTTAAT 582
QY      121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuSerSerAsnValArg 140
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QY      161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db      703 GACTTGTTCATGTCCATAAAATAGCTATGCTCTTGTGTGAGCACAGAACATCACT 762
QY      181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db      763 TATACATTTACGCTGGTGATATAGTCCATGATGGTTTCNAATTGCTGTTCGCTGT 822
QY      201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db      823 GGTGGGCGCGTATTTGCTCTCCAAACAGCGCTGGAGATCGTAGACGGTCCAAGTACCAG 882
QY      221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
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QY      241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
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QY      261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db      1003 GCTGTGCAACGGTTAAGAAAAACATAGCAAGTGGTGGTCCGTTGATTCCTCGTTAAGC 1062
QY      281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
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QY      361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
Db      1303 GCATACATAGAGCAAGGAGGATGAAGAAAGTAAATGAAGTTGGCAGATGCTTTA 1362
QY      381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
Db      1363 GGGTCAGGCTTTAAGTAAACAGTGCAGTTTGGTGGCTCTAAACAAATGTCAAGGTTGG 1422
QY      401 ThrAsnSerProTyrGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
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QY      421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
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RESULT 2
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ID AAD28510 standard; DNA; 1521 BP.
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AC AAD28510;
XX
XX 22-APR-2002 (first entry)
XX
XX A. thaliana FAEL-B. napus elongase KCS chimeric gene, At114 mutant #5.
XX
XX Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
XX very long chain fatty acid; VLCFA; FAEL gene; chimeric; mutant; ds.
XX
XX Chimeric - Arabidopsis thaliana.
OS
XX Chimeric - Brassica napus.
XX
XX Key Location/Qualifiers
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XX WO200194565-A2.
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XX 13-DEC-2001.
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XX 08-JUN-2001; 2001WO-US18737.
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XX 08-JUN-2000; 2000US-210326P.
XX
XX (OYMI-) UNIV MIAMI.
XX
XX Jaworski JG, Blacklock BJ;
XX
XX WPI: 2002-154572/20.
XX
XX P-PSDB; AAEL17618.
XX
XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
XX acids encoding the polypeptide, useful for producing very long chain
XX fatty acids
XX
XX Disclosure; Fig 2-10; 139pp; English.
XX
XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
XX (KCS) polypeptides with altered substrate specificity and/or catalytic
XX activity and nucleic acid molecules encoding such polypeptides.
XX Polypeptides of the invention are useful for catalysing the condensation
XX of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
XX of C20 fatty acyl CoA. They are especially useful for producing very
XX long chain fatty acids (VLCFA) and may be used in the development of
XX reagents for various purposes, e.g., immunological reagents to monitor
XX expression of elongase KCS polypeptides or nucleic acid probes or
XX primers to monitor inheritance of an elongase KCS gene in plant breeding
XX programs. The present sequence is a mutant of Arabidopsis thaliana FAEL-
XX Brassica napus elongase KCS chimeric gene, At114 designated as
XX At114 K92R G307D.
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XX Sequence 1521 BP; 414 A; 341 C; 343 G; 423 T; 0 other;
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XX Alignment Scores:
XX Pred. No.: 7,88e-235 Length: 1521
XX Score: 2243.00 Matches: 431

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Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 1
Query Match: 99.69% Indels: 0
DB: 24 Gaps: 0

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QY 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnIleArgSerGly 60
DB 343 GGCACGGTGTGATTCGTCGTGGCTTGACTTCTTGAGGAAGATTCAAGAAGCTTTCAGGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
DB 403 CTAGGGGATGAAACTCACGGGCCCGAGGGGCTGCTTCAGTGCTCCCGGAAGACTTTT 462
QY 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
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QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
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QY 241 GlnGlyAspAspGluAsnGlnLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
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DT 22-APR-2002 (first entry)
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KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW very long chain fatty acid; VLCFA; FAEL1 gene; chimeric; ds.
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OS Chimeric - Arabidopsis thaliana.
OS Chimeric - Brassica napus.
FH Key
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PN WO200194565-A2.
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XX 13-DEC-2001.
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XX 08-JUN-2001; 2001WO-US18737.
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XX 08-JUN-2000; 2000US-210326P.
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XX Jaworski JG, Blacklock BJ;
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XX WPI: 2002-154572/20.
DR
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XX P-PSDB; AAEL1611.
DR
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XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
XX acids encoding the polypeptide, useful for producing very long chain
XX fatty acids
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XX Disclosure; Fig 2-4; 139pp; English.
PS
XX
XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
XX (KCS) polypeptides with altered substrate specificity and/or catalytic
CC

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CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
 CC of C20 fatty acyl CoA. They are especially useful for producing very
 CC long chain fatty acids (VLCFA) and may be used in the development of
 CC reagents for various purposes, e.g., immunological reagents to monitor
 CC expression of elongase KCS polypeptides or nucleic acid probes or
 CC primers to monitor inheritance of an elongase KCS gene in plant breeding
 CC programs. The present sequence is Arabidopsis thaliana FAEL1-
 CC Brassica napus elongase KCS chimeric gene designated as At114.

XX
 SQ Sequence 1521 BP; 413 A; 342 C; 343 G; 423 T; 0 other;

Alignment Scores:

Pred. No.: 1..3e-234 Length: 1521
 Score: 2241.00 Matches: 430
 Percent Similarity: 99.77% Conservative: 1
 Best Local Similarity: 99.54% Mismatches: 0
 Query Match: 99.60% Indels: 0
 DB: 24 Gaps: 0

SEQ14-JOIN-SEQ4 (1-432) x AAD28503 (1-1521)

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AC AAD28507;
DF 22-APR-2002 (first entry)
XX A. thaliana FAEL-B. napus elongase KCS chimeric gene, At114 mutant #3.
KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
very long chain fatty acid; VLCFA; FAEL gene; chimeric; mutant; ds.
XX Chimeric - Arabidopsis thaliana.
OS Chimeric - Brassica napus.
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XX WO200194565-A2.
XX 13-DEC-2001.
XX 08-JUN-2001; 2001WO-US18737.
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XX 08-JUN-2000; 2000US-210326P.
PR (UYMI-) UNIV MIAMI.
XX Jaworski JG, Blacklock BJ;
PI WPI; 2002-154572/20.
XX P-PSDB; AAE17615.
XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
acids encoding the polypeptide, useful for producing very long chain
fatty acids
XX Disclosure; Fig 2-8; 139pp; English.
XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
(KCS) polypeptides with altered substrate specificity and/or catalytic
activity and nucleic acid molecules encoding such polypeptides.
XX Polypeptides of the invention are useful for catalysing the condensation
of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
of C20 fatty acyl CoA. They are especially useful for producing very
long chain fatty acids (VLCFA) and may be used in the development of
reagents for various purposes, e.g., immunological reagents to monitor
expression of elongase KCS polypeptides or nucleic acid probes of
primers to monitor inheritance of an elongase KCS gene in plant breeding
programs. The present sequence is a mutant of Arabidopsis thaliana FAEL-
Brassica napus elongase KCS chimeric gene, At114 designated as
CC At114 G307D.
XX SQ Sequence 1521 BP; 415 A; 341 C; 342 G; 423 T; 0 other;
Alignment Scores:
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Score: 2240.00 Matches: 430
Percent Similarity: 99.77% Conservative: 1
Best Local Similarity: 99.54% Mismatches: 1
Query Match: 99.56% Indels: 0
DB: 24 Gaps: 0
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Db 223 AATCCGGTTTATCTCGTTGACTACTCTGTTGTTACCTTCCGCCACCCCATCTCAAGTTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
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Qy 61 LeuGlyAspGluThrHisGlyProGluLeuGluValProProArgLysThrPhe 80
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Qy	361	AlaTyrrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu	380
Db	1303	GCATACATAGAAACAAAAGGAAGCATGAAGAAAGGTAAATAAGTTTGGCAGATTGCTTTA	1362
Qy	381	GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer	400
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Qy	401	ThrAsnSerProThrGluHisCysLysLeaspArgTyrrProValLysIleAspSerAspSer	420
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 ID AAD28505 standard; DNA; 1521 BP.
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 AC AAD28505;
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 XX 22-APR-2002 (first entry)
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 DE A. thaliana FAEL-B. napus elongase KCS chimeric gene, At114 mutant #1.
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 KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW Very long chain fatty acid; VLCFA; FAEL gene; chimeric; mutant; ds.
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 XX Chimeric - Arabidopsis thaliana.
 OS Chimeric - Brassica napus.
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 XX Key Location/Qualifiers
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 FT chimeric protein, At114 mutant #1"
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 XX 08-JUN-2001; 2001WO-US18737.
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 XX 08-JUN-2000; 2000US-210326P.
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 XX (UYMI-) UNIV MIAMI.
 PA
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 PI Jaworski JG, Blacklock BJ;
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 XX WPI; 2002-154572/20.
 DR
 DR P-PSDB; AAEL17613.
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 XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids
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 CC primers to monitor inheritance of an elongase KCS gene in plant breeding
 CC programs. The present sequence is a mutant of Arabidopsis thaliana FAEL
 CC Brassica napus elongase KCS chimeric gene, At114 designated as
 CC At114 191C K92R.
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 XX Sequence 1521 BP; 413 A; 341 C; 344 G; 423 T; 0 other;
 SQ
 Alignment Scores:

PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids

XX Disclosure; Fig 2-10; 139pp; English.

XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalyzing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
 CC of C20 fatty acyl CoA. They are especially useful for producing very
 CC long chain fatty acids (VLCFA) and may be used in the development of
 CC reagents for various purposes, e.g., immunological reagents to monitor
 CC expression of elongase KCS polypeptides or nucleic acid probes or
 CC primers to monitor inheritance of an elongase KCS gene in plant breeding
 CC programs. The present sequence is a mutant of Arabidopsis thaliana FAEL-
 CC Brassica napus elongase KCS chimeric gene, At114 designated as
 CC At114 L91C K92R G307D.

XX
 SQ Sequence 1521 BP; 415 A; 340 C; 343 G; 423 T; 0 other;

Alignment Scores:

Pred. No.: 9,75e-234 Length: 1521
 Score: 2233.00 Matches: 429
 Percent Similarity: 99.54% Conservative: 1
 Best Local Similarity: 99.31% Mismatches: 2
 Query Match: 99.24% Indels: 0
 DB: 24 Gaps: 0

SEQ14-JOIN-SEQ4 (1-432) x AAD28509 (1-1521)

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 DB 223 AATCGGTTTATCTCGTTGACTACTCGTTACCTTCGCCGCCGCGATTGCAGAGTAGT 282
 QY 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
 DB 283 GTCTTAAGTCATGGGATATTTCTACCAATATGAAAGCTGATATCTTCCACGGAAC 342
 QY 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
 DB 343 GCGCGATGTGATAATCTCGTGGCTGACTTCTTGGAGGAGATTCGAAGCGTTTCAGT 402
 QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
 DB 403 CTAGCGGATGAATCTACGCGCCGAGGGCTGCTTCAGTCCCTCCCGGAGAGCTTTT 462
 QY 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
 DB 463 GCGGCGCGCGTGAAGAGACGGAGCAAGTTATCATTTGCTGCGCTAGAAAATCTATTCAAG 522
 QY 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
 DB 523 AACACCAACGTTAACCTTAAGATATAGGTATATCTTGGTGAACCAACGATGTTTAAAT 582
 QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
 DB 583 CCAACTCCATCGCTCTCCGCGATGGTCTTAACACTTTCAGCTCCGGAACCAACGTAAGA 642
 QY 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
 DB 643 AGCTTTAACCTTGGTGCATGGTGTAGTCCGCGGCTTATAGCCATGATCTAGCAAG 702
 QY 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
 DB 703 GACTTGTGTGATGTCCATAAAATACGATGCTCTTGTGGTGAGCAGAGAACATCACT 762
 QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
 DB 763 TATACATTTACGCTGGTATATAGTCCATGATGTTCAATTCGTTGTCGCTGTT 822
 QY 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220

DB 823 GGTGGGCGCCCTATTTTGTCTCCAACCAAGCCTGGAGATCGTAGCGGTCCAGTAGCAG 882
 QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
 DB 883 CTAGTTTACACACGGTTTCCAAACGCATACCGGAGCTGACGACAAGTCTTTTTCGTTGGTGCAA 942
 QY 241 GlnGlyAspAspGluAsnGlnLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
 DB 943 CMAGGAGCAGCATGAGNACCGCAAAATCGAGTGAGTTTGTCCAAAGCAGATACACGATGTT 1002
 QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSer 280
 DB 1003 GCTGTCGAACGGTTTAAAGAAAAACATAGCAAGCTTGGTTCGTTGATTTCTTCGTTAAGC 1062
 QY 281 GluLysLeuLeuPhePheValThrPheMetGlyLysIleLysLeuPheLysAspLysLys 300
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 QY 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
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 DB 1303 GCATACATAGAACCAAAAGGAGGATGAGNAGAGTAAAGTTTGGCAGATTGCTTTA 1362
 QY 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer 400
 DB 1363 GGGTCAGGCTTTAAGTGAACAGTGCAGTTTGGGTGGCTCTAAACAATGCTCAAGCTTCG 1422
 QY 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
 DB 1423 ACAATAGTCTTGGAAACACTGCATCGACAGATACCGGTCAAAATGATTCGATTC 1482
 QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
 DB 1483 GGTAAGTCAGACTCGTGTCCAAAACGGTCGGTCC 1518
 RESULT 8
 AAD28504
 ID AAD28504 standard; DNA; 1518 BP.
 XX
 AC AAD28504;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE A. thaliana FAEL-Brassica napus elongase KCS chimeric gene, At74.
 XX Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAEL gene; chimeric; ds.
 XX Chimeric - Arabidopsis thaliana.
 OS Chimeric - Brassica napus.
 FT
 FT Key Location/Qualifiers
 FT CDS 1..1518
 FT /tag= a
 FT /product= "A. thaliana FAEL-Brassica napus elongase KCS
 FT chimeric protein, At74"
 FT
 FT misc_feature 1..222
 FT /tag= b
 FT /note= "Arabidopsis thaliana FAEL gene"
 FT misc_feature 223..1518
 FT /tag= c

FT XX /note= "Brassica napus elongase KCS gene"

PN WO200194565-A2.

PD 13-DEC-2001.

PF 08-JUN-2001; 2001WO-US18737.

PR 08-JUN-2000; 2000US-210326P.

XX (UYMI-) UNIV MIAMI.

XX Jaworski JG, Blacklock BJ;

XX WPI: 2002-154572/20.

DR P-PSDB; AAE17612.

XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
PT acids encoding the polypeptide, useful for producing very long chain
PT fatty acids

PS Disclosure; Fig 2-5; 139pp; English.

XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
CC (KCS) polypeptides with altered substrate specificity and/or catalytic
CC activity and nucleic acid molecules encoding such polypeptides.
CC Polypeptides of the invention are useful for catalysing the condensation
CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
CC of C20 fatty acyl CoA. They are especially useful for producing very
CC long chain fatty acids (VLCFA) and may be used in the development of
CC reagents for various purposes, e.g., immunological reagents to monitor
CC expression of elongase KCS polypeptides or nucleic acid probes or
CC primers to monitor inheritance of an elongase KCS gene in plant breeding
CC programs. The present sequence is Arabidopsis thaliana FAEL-
CC Brassica napus elongase KCS chimeric gene designated as At74.

XX SQ Sequence 1518 BP; 415 A; 343 C; 344 G; 416 T; 0 other;

Alignment Scores:

Pred. No.: 5,72e-230 Length: 1518
Score: 2198.50 Matches: 423
Percent Similarity: 98.84% Conservative: 3
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 97.71% Indels: 1
DB: 24 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x AAD28504 (1-1518)

Qy 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProProHisLeuAtgValSerVal 21
Db 226 CCGTTTACTCGTTGAGTACTCATGCTACCTTCCACCAACCCATTGTAGATCAAGTATC 285
Qy 22 SerLysValMetAspPheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
Db 286 TCCAAAGTGCATGGATATCTTTATCAAGTAAAGAAAGCTGAT--CCTTCTCGGAAGCGC 342
Qy 42 ThrCysAspAspSerSerTrpLeuAspPheLeuAtgLysIleGlnGluAtgSerGlyLeu 61
Db 343 ACGTGGCGATGACTCTCGTGGCTTGACTTCTTGAGGAAGATTCAGAAGCTTCAGGTCTA 402
Qy 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
Db 403 GCGGATGAACCTACAGGCGCGAGGGGCTGCTTTCAGGTCCCTCCCGGAAGACTTTTGGC 462
Qy 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuLysAsn 101
Db 463 GCGGCGGTGAGAGACGCGACAGTATCATTTGGTGGCTAGAAAATCTATTCAAGAAC 522
Qy 102 ThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnPro 121
Db 523 ACCAAGCTTAACCCCTAAAGATATAGTATACTTTGGTGGTGAACCTCAAGCATGTTTAAATCCA 582
Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141

Db 583 ACTCCATCGCTCTCCCGCATGCTGTTAAACACTTTCAGCTCGAAGCAACGTAAGAAGC 642
Qy 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db 643 TTTAACTTGGTGGCATGGTTGTAGTCCGCGCTTATAGCCATTGATCTAGCAAGGAC 702
Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
Db 703 TTGTTGCATGTCATAAAATACGTATGCTCTTGTGTGACACAGAGAACATCATCTAT 762
Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
Db 763 AACATTACGCTGGTATATAGGTCCATGATGCTTCAAAATGCTTGTTCGCTGTGGT 822
Qy 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 823 GGGGCCCTATTTTGTCTCCCAACAGCCTGGAGATCGTAGACGGTCCCAAGTACAGCTA 882
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 883 GTTCACAGCTTTCGAACGCATACCGGAGCTCACGGCAAGTCTTTTTCGTTGCGTGAACAA 942
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db 943 GGAGACGATGAGAACCGCAAAATCGAGTGTGTTGTCGAAGGACATAACCGATTTGCT 1002
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
Db 1003 GGTCAACGGTTAAGAAAAACATACCAACGTTGGTCCGTTGATTCTCCGTTAAGCGAG 1082
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
Db 1063 AAACCTCTTTTTCGTTACCTTCATGGCGAAGAACTTTTCAAGATAAATCAACAT 1122
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
Db 1123 TACTACGTCGCGGATTTCAAACTTGCTATTGACCATTTTGTATACATGCCGGAGCGAGA 1182
Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db 1183 GCCGTGATTGATGTGTAGAGAAACCTAGCCCTAGCAGCGATCGATGTAGAGGCATCA 1242
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleThrTyrGluLeuAla 361
Db 1243 AGATCAACGTTTACATAGATTTGGAACACACTTCATCTAGCTCAATATGATGATGGCA 1302
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
Db 1303 TACATAGAACCAAGAGGAGGATGAAGAAAGGTAAATAAGTTTGGCAGATTGCTTTAGGG 1362
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401
Db 1363 TCAGGCTTTAAGTGTAAACAGTGCAGCTTTGGTGGCTCTTAACCAATGTCAAAGCTTCGACA 1422
Qy 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
Db 1423 AATAGTCTCTGGGAACACTGCATCGACAGATACCGGTCACAAATTCATTCATTCAGGT 1482
Qy 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 AAGTCAGAGACTCGTGTCTCCAAACCGTCGGTCC 1515
RESULT 9
AAD28501
ID AAD28501 standard; DNA; 1524 BP.
XX
AC AAD28501;
XX
DT 22-APR-2002 (first entry)
XX
DE Brassica napus fatty acid elongase KCS encoding DNA #1.
XX

KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; ds.
 XX Brassica napus.
 XX Key Location/Qualifiers
 FH 1..1521
 FT CDS /*tag= a
 FT /product= "Brassica napus fatty acid elongase KCS
 FT protein #1"
 XX
 XX W0200194565-A2.
 XX
 XX 13-DEC-2001.
 XX
 XX 08-JUN-2001; 2001WO-US18737.
 XX
 XX 08-JUN-2000; 2000US-210326P.
 XX
 XX (UYMI-) UNIV MIAMI.
 XX
 XX Jaworski JG, Blacklock BJ;
 XX
 XX WPI: 2002-154572/20.
 DR P-PSDB: AAEI7609.
 XX
 XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids
 XX
 XX Example 1; Fig 2-2; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
 CC of C20 fatty acyl CoA. They are especially useful for producing very
 CC long chain fatty acids (VLCFA) and may be used in the development of
 CC reagents for various purposes, e.g., immunological reagents to monitor
 CC expression of elongase KCS polypeptides or nucleic acid probes or
 CC primers to monitor inheritance of an elongase KCS gene in plant breeding
 CC programs. The present sequence is Brassica napus fatty acid elongase KCS
 CC encoding DNA.
 XX
 SQ Sequence 1524 BP; 421 A; 350 C; 344 G; 409 T; 0 other;

Alignment Scores:
 Pred. No.: Length: 1524
 Score: 2198.50 Matches: 423
 Percent Similarity: 98.84% Conservative: 3
 Best Local Similarity: 98.14% Mismatches: 4
 Query Match: 97.71% Indels: 1
 DB: 24 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x AAD28501 (1-1524)

QY 2 ProValTyrLeuValAspTyrSerCysTyrIleuProProHisLeuArgValSerVal 21
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 Db 229 CCGGTTTACCTCGTTGAGTACTCATGCTTACCTCCACCAACGCATTTGATCAAGTATC 288
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 QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41
 |||||
 Db 289 TCCAAAGTCATGATATCTTTATCAAGTAAAGAGCTGAT--CCCTCTCGGAACGGC 345
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 QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnIleuArgSerGlyLeu 61
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 Db 346 ACGTGCCATGACGTCGTCGGCTTACCTCTTGAGGAAGATTCAAGAAGCTTCAGGTCCTA 405
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 QY 62 GlyAspGlnThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
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 Db 406 GCGCATGAACCTACCGGCGCCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTGGC 465
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QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyValAlaLeuGluAsnLeuPheLysAsn 101
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 Db 466 GCGGCCGCTGAAGACGAGCGAGAGTTATCATTTGGTGGCTAGAAATCTATTTCAGAAC 525
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 QY 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
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 QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
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 Db 766 AACATTTACGCTGGTGATAATAGTCCATGATGTTTCAAAATTCCTTCCGTGTTGGT 825
 |||||
 QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
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 Db 826 GGGGCCGCTATTGCTCTCCAAACGCTGGAGATCGTAGACGCTCCAAAGTACGAGCTA 885
 |||||
 QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
 |||||
 Db 886 GTTCACACGGTTCGAACGCATACCCGAGCTGACGCAAGTCTTTTCGTTGCGTGCAACAA 945
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 QY 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
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 Db 1186 CCCGTGATTGATGTGTAGAGAAGAACTAGCCCTAGCACCGATCGATGATAGAGCATCA 1245
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AAD28508
ID AAD28508 standard; DNA; 1518 BP.
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AC AAD28508;
XX
DT 22-APR-2002 (first entry)
XX
DE A. thaliana FAEL-B. napus elongase KCS chimeric gene, At74 mutant #1.
XX
KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW very long chain fatty acid; VLCFA; FAEL gene; chimeric; mutant; ds.
XX
OS Chimeric - Arabidopsis thaliana.
OS Chimeric - Brassica napus.
XX
FH Key Location/Qualifiers
FT CDS 1..1518
FT FT
FT FT
FT FT
FT misc_feature 1..222
FT FT
FT misc_feature 223..1518
FT FT
FT mutation replace (917, G)
FT FT
XX WO200194565-A2.
XX
XX 13-DEC-2001.
XX
XX 08-JUN-2001; 2001WO-US18737.
XX
XX 08-JUN-2000; 2000US-210326P.
XX
XX (UYMI-) UNIV MIAMI.
XX
XX Jaworski JG, Blacklock BJ;
XX
XX WPI; 2002-154572/20.
XX P-PSDB; AAE17616.
XX
XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
XX acids encoding the polypeptide, useful for producing very long chain
XX fatty acids -
XX
XX Disclosure; Fig 2-9; 139pp; English.
XX
XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
XX (KCS) polypeptides with altered substrate specificity and/or catalytic
XX activity and nucleic acid molecules encoding such polypeptides.
XX Polypeptides of the invention are useful for catalysing the condensation
XX of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
XX of C20 fatty acyl CoA. They are especially useful for producing very
XX long chain fatty acids (VLCFA) and may be used in the development of
XX reagents for various purposes, e.g., immunological reagents to monitor
XX expression of elongase KCS polypeptides or nucleic acid probes or
XX primers to monitor inheritance of an elongase KCS gene in plant breeding
XX programs. The present sequence is a mutant of Arabidopsis thaliana FAEL-
XX Brassica napus elongase KCS chimeric gene, At74 designated as At74 G306D.
XX
XX Sequence 1518 BP; 416 A; 343 C; 343 G; 416 T; 0 other:
XX
Alignment Scores:
Pred. No.: 3 33e-229 Length: 1518
Score: 2191.50 Matches: 422
Percent Similarity: 98.61% Conservative: 3
Best Local Similarity: 97.91% Mismatches: 5
Query Match: 97.40% Indels: 1
DB: 24 Gaps: 1

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SEQ14-JOIN-SEQ4 (1-432) x AAD28508 (1-1518)
QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
DB 226 CCGGTTTACCTCGTTGAGTACTCATCTCCACCAACGATTTGTAGATCAAGTATC 285
QY 22 SerLysValMetAspPheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
DB 286 TCCAGGTGATGATATCTTTTCAAGTAGAAGAACTGAT---CCTTCTCGGAACGGC 342
QY 42 ThrCysAspSerSerTrpLeuAspPheLeuArgLysIleGlnIuArgSerGlyLeu 61
DB 343 ACGTCCGATGACTCGTCGTGGCTTACTCTTGAGGAAGATTCAAGAAGCTTTCAGCTCTA 402
QY 62 GlyAspGluThrHisGlyProGluGlyLeuGlnValProArgLysThrPheAla 81
DB 403 GCGGATGAACTCACGGGCCCGAGGGGCTGCTCAGGTCCCTCCCGGAAGACTTTTGG 462
QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnIlePheLysAsn 101
DB 463 GCGGCGGTGAAGAGACGGCAAGTATCATTTGTCGCTAGAAAATCTATTCAAGAAC 522
QY 102 ThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnPro 121
DB 523 ACCAAGCTTAACCTCAAGATATAGTATACTTGTGTGAACCTCAAGCATGTTTAAATCCA 582
QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
DB 583 ACTCCATCGCTCTCCGGATGGTGTAACTTTCAAGCTCCGAAGCAACGTAAGAAGC 642
QY 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaLeuAspLeuAlaLysAsp 161
DB 643 TTTAACTTTGGTGGCATGGGTTGTAGTCCGCGGTTATAGCCATTGATCTAGCAAGGAC 702
QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
DB 703 TTGTTGCATGTCATAAAATACGTATGCTCTGTGTGGACACAGAACATCATTAT 762
QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
DB 763 AACATTTACGCTGGTGATATAGTCCATGATGGTTTCMAATTTGTTGCTCGTGTGT 822
QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
DB 823 GGGCGCGTATTTTCTCTCCAAAGCCTGGAGATCGTAGCGTCCCAAGTACAGGCTA 882
QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
DB 883 GTTCACAGGTTTCAAGCATACCGGAGCTGACGACAAGTCTTTTTCGTTGCGTCAACAA 942
QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
DB 943 GGAGACGATGAGACGGCAAAATCGGAGTGAGTTGTCCAAAGGACATACCGATGTGCT 1002
QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
DB 1003 GGTCTGAACGGTTAAGAAAAACATAGCAAGTGGGTGCGTGTGATCTTCGTTTAACGGAG 1062
QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
DB 1063 AAACCTCTTTTTCGTTACCTTCATCGGCAAGAAACATTTTCAAGATAAATCAACAT 1122
QY 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
DB 1123 TACTACGTCGCGGATTTCAAACTTGCTATTTGACCATTTTGTATACATGCCGAGCAGA 1182
QY 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleLeuAspValGluAlaSer 341
DB 1183 GCGGTGATGTGCTAGAGAGACCTAGCCCTAGCAGCATCGATGTAGAGCATCA 1242
QY 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrTyrGluLeuAla 361
DB 1243 AGATCAACGTTACATAGATTGGAAACACTTCTATCTAGCTCAATATGATGATGGCA 1302

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QY 362 TvrileGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
 Db 1303 TACATAGAACCAAGGAGGAGGTGAAGAAAGGTAATAAGATTGGCAGATTGCTTTAGGG 1362

QY 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401
 Db 1363 TCAGGCTTTAAGTGTAAACAGTGCAGTTGGTGGCTCTAAACAATGTCAAGCTTCGACA 1422

QY 402 AsnSerProTrpGluHisCysIleAspAtgTyrProValLysIleAspSerAspSerGly 421
 Db 1423 AATAGTCTTGGACACTGCATGCACAGATACCCGGTCAAAATGTATTCTGATTGAGGT 1482

QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
 Db 1483 AAGTCAGAGACTCGTGTCCAAACGGTTCGGTCC 1515

RESULT 11
 AAD28516
 ID AAD28516 standard; DNA; 1524 BP.
 XX AC AAD28516;
 XX XX
 DT 22-APR-2002 (first entry)
 XX
 DE Brassica napus fatty acid elongase KCS DNA #1 mutant, Bn G307D.
 XX
 DE Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; mutant; ds.
 KW
 XX OS Brassica napus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1521
 FT FT /*tag= a
 FT FT /product= "Brassica napus fatty acid elongase KCS
 FT FT protein #1 mutant Bn G307D"
 FT FT replace (920, G)
 FT FT /*tag= b
 XX
 PN WO200194565-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 08-JUN-2001; 2001WO-US18737.
 XX
 PR 08-JUN-2000; 2000US-210326P.
 XX
 PA (UYMI-) UNIV MIAMI.
 XX
 PI Jaworski JG, Blacklock BJ;
 XX
 DR WPI; 2002-154572/20.
 DR P-PSDB; AAE17624.
 XX
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids
 XX
 PS Disclosure; Fig 2-17; 139pp; English.
 XX
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
 CC of C20 fatty acyl CoA. They are especially useful for producing very
 CC long chain fatty acids (VLCFA) and may be used in the development of
 CC reagents for various purposes, e.g., immunological reagents to monitor
 CC expression of elongase KCS polypeptides or nucleic acid probes or
 CC primers to monitor inheritance of an elongase KCS gene in plant breeding
 CC programs. The present sequence is a mutant of Brassica napus fatty acid
 CC elongase KCS protein #1 encoding DNA designated as Bn G307D.

XX SQ Sequence 1524 BP; 422 A; 350 C; 343 G; 409 T; 0 other;
 Alignment Scores:
 Pred. No.: 3,35e-229 Length: 1524
 Score: 2191.50 Matches: 422
 Percent Similarity: 98.61% Conservative: 3
 Best Local Similarity: 97.91% Mismatches: 5
 Query Match: 97.40% Indels: 1
 DB: 24 Gaps: 1
 SEQ14-JOIN-SEQ4 (1-432) x AAD28516 (1-1524)
 QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
 Db 229 CCGGTTTACCTCGTTCAGTACTCATCTCCACCAACGCAATGTAGATCAAGTATC 288
 QY 22 SerLysValMetAspPheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
 Db 289 TCCAAGGTCTATGATATCTTTTATCAAGTAAGAAAGCTGAT---CCTTCTCGGAACGCG 345
 QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
 Db 346 ACGTGGCATGACTCGTCTGGCTTGCATCTCTTGAGGAAGATTCAAGACGTTCAAGTCTA 405
 QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
 Db 406 GCGGATGAAACTCACGGGCCCGAGGGGCTGCTTCAGGTCCTCCCGGAAGACTTTTTCG 465
 QY 82 AlaAlaArgGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
 Db 466 GCGGCGGTGAAGACGAGGCAAGTTATCATTTGTCGCTAGAAATCTATTCAAGAAC 525
 QY 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
 Db 526 ACCAACGTTTAACCTTAAGATATAGGTATCTTGTGGTAACCTCAAGCATGTTTAATCCA 585
 QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
 Db 586 ACTCCATCGCTCTCCGCGATGCTGTTAACTTCAAGCTCCGAAGCAACGTAAGAAGC 645
 QY 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
 Db 646 TTTAACCTTGTGGCATGGGTTGTAGTGCGGCGTTATAGCCATTGATCTAGCAAGAC 705
 QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
 Db 706 TTGTTGCATGTCCATAAAAAATACGTATGCTCTTGTGTGAGCAGACAGACATCACTTAT 765
 QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 Db 766 AACATTTACCTGGTGATTAATAGTTCATGTTTCAAAATGCTTGTTCGGTGGTGGT 825
 QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
 Db 826 GGGCGCGCTATTGCTCTCCAAACAGCCTGGAGATCGTAGAGGTCCCAAGTACAGCTA 885
 QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
 Db 886 GTTCACACGGTTGCAACGATACCGAGCTACGACACAGTCTTTTCGTTGGTGCAACAA 945
 QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
 Db 946 GGAGACGATGAGAAGCGGAAAAATCGAGTGGATTGTTCCAAAGACATAACCGATGTTGCT 1005
 QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
 Db 1006 GGTTCGACGGTTAAGAAAAACATAGCAACGTTGGTGGCTGATTCTTCCTCGTTAAGCGAG 1065
 QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
 Db 1066 AAACCTCTTTTGTGTTACCTTCATGGCAAGAAACTTTTCAAGAGATAAAATCAACAT 1125

Db 891 GGTGCAACGGTTAAGAAAAACATAGCAACGGTTGGGTGGTTCGTTGATTCTTCGTTAAGCGAG 950
 QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLeuLysHis 301
 Db 951 AACTCTCTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAGATAAAATCAAAACAT 1010
 QY 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
 Db 1011 TACTACGTCGCGGATTTCAAACTTGCTATTGACCATTTTGTATACATGCGGAGGCGAGA 1070
 QY 322 AlaValIleAspValLeuGlyLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
 Db 1071 GCGGTGATGTGCTAGAGAAACCTTAGCCCTAGCCAGATCGATGATGATGATGATGATCA 1130
 QY 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerSerSerSerSerSerSer 361
 Db 1131 AGATCAACGTTTACATAGATTGTTGAAACACTTCATCTAGCTCAATATGATGATGATGATG 1190
 QY 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
 Db 1191 TACATAGAAGCAAAAGGATGAAGAAGTAATAAAGTTGGCAGATGCTTTAGGG 1250
 QY 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr 401
 Db 1251 TCAGGCTTTAAGTGTAAAGTACAGTGCAGTTTGGGTGGCTCTAAACATATGTCAAGCTTCGACA 1310
 QY 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
 Db 1311 AATAGTCTCTGGGAACACTGCATCGACAGATACCGGTCAAAATGATTCGTATCAGGT 1370
 QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
 Db 1371 AAGTCAGAGACTCGTGTCCAAAACGTCGGTCC 1403

RESULT 13
 AAF61744
 ID AAF61744 standard; cDNA; 1785 BP.
 AC AAF61744;
 XX
 DT 12-JUL-2001 (first entry)
 DE B. napus KCS cDNA SEQ ID 1.
 XX
 KW KCS; beta-ketoacyl-CoA-synthase; transgenic plant; long-chain fatty acid;
 KW cleaning composition; cosmetic; dye additive; lubricant; preservative;
 KW plasticizer; seed-specific expression; fatty acid biosynthesis;
 KW lipid metabolism; ss.
 XX
 OS Brassica napus.
 XX
 PN WO200129238-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 20-OCT-2000; 2000WO-EP10363.
 XX
 PR 20-OCT-1999; 99DE-1050589.
 XX
 PA (ERWE-) GES ERWERB & VERW VON SCHUTZRECHTEN-GVS.
 XX
 PI Wolter FP, Han J, Frentzen M;
 XX
 DR WPI; 2001-273877/28.
 XX
 PT New nucleic acid encoding beta-ketoacyl-CoA-synthase from Brassica
 PT napus, useful for preparing transgenic plants with high content of very
 PT long, optionally unsaturated, fatty acids -
 XX
 PS Claim 2; Page 54-55; 59pp; German.
 XX
 CC This invention describes a novel nucleic acid (I) encoding a protein
 CC (II), from Brassica napus, with beta-ketoacyl-CoA-synthase (KCS)

CC activity. (I) is used to generate transgenic plants or microorganisms
 CC with increased content of long-chain fatty acids, especially increased
 CC ratio of 22:1 to 20:1, relative to the wild type. These fatty acids are
 CC variously useful as (or for producing) e.g. cleaning compositions,
 CC cosmetics, dye additives, lubricants, preservatives, plasticizers etc.
 CC Where the fatty acids are polyunsaturated, they are also useful in
 CC nutrition and pharmaceuticals. A promoter (Ia), from (I), is used to
 CC provide seed-specific expression of other genes linked to it,
 CC particularly those involved in fatty acid biosynthesis or lipid
 CC metabolism, but also for 'switching off' selected genes by antisense or
 CC co-suppression methods. (I), encoding an enzyme that catalyzes elongation
 CC of fatty acid chains, increases the proportion of the more valuable
 CC longer chain fatty acids at the expense of shorter chain acids. A vector
 CC containing the napin promoter; the KCS sequence of B. napus and the polyA
 CC signal from the same gene, was used to transform the low-erucic acid rape
 CC variety Drakkar. The fatty acid distribution of one selected F2 line was
 CC 7.3% 20:1; 5.6% 22:1 and 0.4% 24:1, i.e. 13.3 wt.% total very long chain
 CC fatty acids. Comparable figures for the parent variety were 1.9%; 0.1%
 CC and 0.3% (2.3% total). This sequence encodes a Brassica napus KCS protein
 CC described in the method of the invention.

SQ Sequence 1785 BP; 507 A; 394 C; 381 G; 503 T; 0 other;

Alignment Scores:

Pred. No.: 4 23e-229 Length: 1785
 Score: 2191.50 Matches: 422
 Percent Similarity: 98.61% Conservative: 3
 Best Local Similarity: 97.91% Mismatches: 5
 Query Match: 97.40% Indels: 1
 DB: 22 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x AAF61744 (1-1785)

QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
 Db 310 CCGGTTTACCTCGTTGAGTACTCATGCTCTCCACCAACGCAATGTAGATCAAGTATC 369
 QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
 Db 370 TCCAAGGTCATGATATCTTTTATCAAGTAAGAAGAGCTGAT---CCTTCTCGGAACGGC 426
 QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnArgSerGlyLeu 61
 Db 427 ACGTGGGATGACTCGTGTGGCTTGACTTCTTGAGGAAGATTCAGAAGCTTCAGGTCTA 486
 QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProArgLysThrPheAla 81
 Db 487 GCGGATGAACCTACGGGCGCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTGGC 546
 QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
 Db 547 GCGGCGCGTGAAGACGACGAGCAAGTTATCATTTGGTGGCTAGAAAAATCTATTCAAGAAC 606
 QY 102 ThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnPro 121
 Db 607 ACCACGTTTAAACCTTAAAGATATAGGTATCTTGTGCTGAACCTCAAGCATGTTTATCCA 666
 QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
 Db 667 ACTCCATGCTCTCCCGCATGGTGTTCACACATTTCAAGCTCCGGAAGCAAGCTAAGAAGC 726
 QY 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
 Db 727 TTTTAACTTTGGTGGCATGGGTTGTAGTCCGCGCTTATAGCCATTGATCTAGCAAGGAC 786
 QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
 Db 787 TTGTTGCATGTCCTCAAAAATACGATGCTCTTGTTGGTGAGCACAGACATCATTAT 846
 QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 Db 847 AACATTAGCTGGTGATTAATAGGTCCATGATGTTTCAAAATGCTTCTCCGTTGGT 906

```
Qy 202 GlyAlaAlaLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 907 GGGGGCGCTATTTCCTCCAAAGCCTGGAGATCGTAGCGGTCCAAAGTACGAGCTA 966
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 967 GTTCACAGGTTCGACCGCATACCGAGCTGACGACAGTCTTTTCGTCGTCACAA 1026
Qy 242 GlyAspAspGluAsnGlyLysLysGlyValSerLysSerLysAspLysLeuThrAspValAla 261
Db 1027 GGAGAGCATGAGAAACCGCAAAATCGGAGTCAGTTTCTCCAAAGGACATAAACCGATGTGCT 1086
Qy 262 GlyArgThrValLysLysAsnLysAlaThrLeuGlyProLeuLeuLeuProLeuSerGlu 281
Db 1087 GGTGCAACGGTTAAGAAACATAGCAACGTTGGGTCCGTTGATTCTTCGTTAAACGGAG 1146
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLysLeuPheLysAspLysLysHis 301
Db 1147 AACTTCTTTTTCGTTACCTTTCATGGCAAGAACTTTTCAAGATATAAATCAAAACAT 1206
Qy 302 TyrTyrValProAspPheLysLeuAlaLysPheHisPheCysLysLysAlaGlyGlyArg 321
Db 1207 TACTAGTCCCGATTTCAAACTTGCTATTGACCATTTTGTATACATGCGCGAGGCAGA 1266
Qy 322 AlaValLysAspValLeuGlyLysAsnLeuAlaLeuAlaProLysAspValGluAlaSer 341
Db 1267 GCGGTGATTGATGCTAGAGAAACCTAGCCCTAGCACCGATCGATGTAGAGGCATCA 1326
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerLysLysLysLysLysLys 361
Db 1327 AGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTAGCTCAATATGTTAGTTGGCA 1386
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnLysLeuGly 381
Db 1387 TACATAGAGCAAGAAAGGATGAGAAAGGTAATAAGATTGGCAGATTGCTTTAGGG 1446
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401
Db 1447 TCAGGCTTTTAAGTGAACAGTGCAGTTGGGTGGCTCTAAACAATGTCAAAGCTTCGACA 1506
Qy 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysLysLysAspSerAspSerGly 421
Db 1507 AATAGTCTTGGGACACATGCTGCACAGATACCCGGTCAAAATTGATTCTGATTACAGT 1566
Qy 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1567 AAGTCAGAGACTCGTGTCCAAACGGTCCGTCC 1599
RESULT 14
AAF61746
ID AAF61746 standard; cDNA; 1785 BP.
XX
AC AAF61746;
XX
XX 12-JUL-2001 (first entry)
XX
XX B. napus KCS cDNA SEQ ID 3.
XX
KW KCS; beta-ketoacyl-CoA-synthase; transgenic plant; long-chain fatty acid;
KW cleaning composition; cosmetic; dye additive; lubricant; preservative;
KW plantcizier; seed-specific expression; fatty acid biosynthesis;
KW lipid metabolism; ss.
XX
XX Brassica napus.
XX
XX Key Location/Qualifiers
XX CDS 82..1602
XX /*tag= a
XX /product= "KCS"
XX
XX WO200129238-A2.
XX
XX 26-APR-2001.
```

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XX
PF 20-OCT-2000; 2000WO-EP10363.
XX
PR 20-OCT-1999; 99DE-1050589.
XX
XX (ERWE-) GES ERWERB & VERW VON SCHUTZRECHTEN-GVS.
XX
PI Wolter FP, Han J, Frentzen M;
XX
DR WPI; 2001-273877/28.
DR P-PSDB; AAB70888.
XX
PT New nucleic acid encoding beta-ketoacyl-CoA-synthase from Brassica
PT napus, useful for preparing transgenic plants with high content of very
PT long, optionally unsaturated, fatty acids.
XX
XX Claim 2; Fig 1; 59pp; German.
XX
CC This invention describes a novel nucleic acid (I) encoding a protein
CC (II), from Brassica napus, with beta-ketoacyl-CoA-synthase (KCS)
CC activity. (I) is used to generate transgenic plants or microorganisms
CC with increased content of long-chain fatty acids, especially increased
CC ratio of 22:1 to 20:1, relative to the wild type. These fatty acids are
CC variously useful as (or for producing) e.g. cleaning compositions,
CC cosmetics, dye additives, lubricants, preservatives, plasticizers etc.
CC Where the fatty acids are polyunsaturated, they are also useful in
CC nutrition and pharmaceuticals. A promoter (Ia), from (I), is used to
CC provide seed-specific expression of other genes linked to it,
CC particularly those involved in fatty acid biosynthesis or lipid
CC metabolism, but also for 'switching off' selected genes by antisense or
CC co-suppression methods. (I), encoding an enzyme that catalyzes elongation
CC of fatty acid chains, increases the proportion of the more valuable
CC longer chain fatty acids at the expense of shorter chain acids. A vector
CC containing the napin promoter; the KCS sequence of B. napus and the polyA
CC signal from the same gene, was used to transform the low-erucic acid rape
CC variety Brakkar. The fatty acid distribution of one selected T2 line was
CC 7.3% 20:1; 5.6% 22:1 and 0.4% 24:1, i.e. 13.3 wt.% total very long chain
CC fatty acids. Comparable figures for the parent variety were 1.9%; 0.1%
CC and 0.3% (2.3% total). This sequence encodes a Brassica napus KCS protein
CC described in the method of the invention.
XX
SQ Sequence 1785 BP; 507 A; 394 C; 381 G; 503 T; 0 other;
```

```
Alignment Scores:
Pred. No.: 4,23e-229 Length: 1785
Score: 2191.50 Matches: 422
Percent Similarity: 98.61% Conservative: 3
Best Local Similarity: 97.91% Mismatches: 5
Query Match: 97.40% Indels: 1
DB: 22 Gaps: 1
```

SEQ14-JOIN-SEQ4 (1-432) x AAF61746 (1-1785)

```
Qy 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLysLeuArgValSerVal 21
Db 310 CCGGTTTACCTCGTGTGACTACTGCTACCTCCCAACGACATGTAGATCAAGATATC 369
Qy 22 SerLysValMetAspPheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41
Db 370 TCCAGGTGATGGATATCTTTATCAAGTAGAANAAGCTGAT---CCTTCTCGGAACGGC 426
Qy 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysLysLysGlnGluArgSerGlyLeu 61
Db 427 ACGTGGCATGATCGTGTGCTGCTGCTTCTTCTGAGGAAGATTCGAAGAAGCTTCAGTCTA 486
Qy 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
Db 487 GCGGATGAACACTACGCGCCCGAGGGGCTGCTTCAGGTCCCTCCCGGAGACTTTTGGC 546
Qy 82 AlaAlaArgGluGluThrGluGlnValLlelleGlyAlaLeuGluAsnLeuPheLysAsn 101
Db 547 GCGGCGGTGAAGAGACGGAGCAAGTTATCATTTGCTGCTAGAAAATCTATTATCAAGAAC 606
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Qy 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
Db 607 ACCAAGTAAACCTTAAGATATAGTATATCTGGTGAACCTCAAGCATGTTTAAATCCA 666
Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
Db 667 ACTCCATCGCTCTCGCGATGGTGGTAAACACTTTCAAGCTCCGAAGCAACGTAAGAAGC 726
Qy 142 PheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db 727 TTTAACCTTGGTGGCATGGTGTAGTCCGGCGGTATAGCCATGTATAGCAAGAGAC 786
Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
Db 787 TTGTTGCATGTCCATAAAATAGTATGCTCTGTGGTGACACAGAGAACATCACTTAT 846
Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
Db 847 ACATTTACGCTGGTGATATAGTCCATGATGGTTTCAANTTGGTTCGCTGGTGGT 906
Qy 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 907 GGGGCGCTATTTGCTCTCCACAGCCTGGAGATCGTACCGTCCAAAGTACGAGCTA 966
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 967 GTTACACGGTTCGAACGATACCGGAGCTGACGACAAGTCTTTTCGTTCCGTGCAACAA 1026
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db 1027 GGAGACGATAGAACGCAAAATCGGAGTGAGTTGTCCAAAGGACATTAACCGATGTGCT 1086
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
Db 1087 GGTCAACGGTAAAGAAAACATAGCAACGTTGGTGGTGGTATCTTCGTTAACCAG 1146
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLysHis 301
Db 1147 AAATCTCTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAGATAAAATCAAAACAT 1206
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
Db 1207 TACTACGTCCCGGATTTCAACCTTGCTATGTACCATTTTGTATACATCGCGAGGACGA 1266
Qy 322 AlaValIleAspValLeuGlyLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db 1267 GCCGTGATTGATGCTAGAGAGAACCTTAGCCCTAGCACCAGATCGATGTAGAGGCATCA 1326
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleThrTyrGluLeuAla 361
Db 1327 AGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGATGATGGTGGCA 1386
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
Db 1387 TACATAGAAGCAAAAGGAGATGAAGAGGTAATAAGTTGGCAGATGCTTTAGGG 1446
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401
Db 1447 TCAGGCTTTAAGTGAACAGTCGAGTTGGTGGCTCTAAACAATGTCAAAGCTTCGACA 1506
Qy 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
Db 1507 AATAGTCTTTGGGAACACTGCATCGACAGATACCCGGTCAAAATGATTCCTGATTCAGGT 1566
Qy 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1567 AAGTCAGAGACTCGTGTCCAAAACGGTGGTCC 1599
RESULT 15
AAF62741
ID AAF62741 standard; DNA; 1790 BP.
XX
AC AAF62741;
```

```
XX
DT 02-MAY-2001 (first entry)
XX
DE Brassica napus FAEL promoter.
XX
KW Brassica napus; FAEL; fatty acid elongation 1;
KW seed-specific gene expression; transgenic plant; seed development;
KW seed lipid metabolism; ds.
XX
OS Brassica napus.
XX
PN WO200111061-A2.
XX
PD 15-FEB-2001.
XX
PF 04-AUG-2000; 2000WO-CA00907.
XX
PR 04-AUG-1999; 99US-0147133.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Kunst L, Clemens S;
XX
WPI; 2001-191548/19.
XX
DR Recombinant nucleic acid for mediating seed-specific expression in
PT Arabidopsis, comprises a heterologous promoter with a transcriptional
PT regulatory region of the 5' region of a plant fatty acid elongation 1
PT gene
XX
PS Disclosure; Fig 2; 41pp; English.
XX
CC The present sequence is the promoter of the Brassica napus FAEL
CC (fatty acid elongation 1) gene. Nucleic acid constructs comprising
CC transcriptional regulatory regions homologous to plant FAEL promoters may
CC be used in transgenic cells or plants to promoter expression of foreign
CC and endogenous genes in developing seeds. The constructs are used to
CC promote expression of foreign and endogenous genes in developing seeds,
CC to affect seed lipid metabolism, protein or carbohydrate composition and
CC accumulation, or seed development. Transcriptional regulatory regions of
CC the FAEL gene may be useful for the production of modified seeds
CC containing novel recombinant proteins which have pharmaceutical,
CC industrial or nutritional value. The nucleic acids may also be used as
CC plant breeding tools, as molecular markers to aid in plant breeding
CC programmes. Such techniques include using the gene as a molecular probe
CC or using the DNA sequence to design PCR primers for use in screening
CC techniques.
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SQ Sequence 1790 BP; 494 A; 401 C; 384 G; 511 T; 0 other;

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2003, 15:22:35 : Search time 2415 Seconds
(without alignments)
5205.968 Million cell updates/sec

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Perfect score: 2255
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	2238	99.2	1521	6	AX358177	Sequence
5	2235	99.1	1521	6	AX358171	Sequence
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ALIGNMENTS

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DEFINITION Sequence 11 from Patent WO0194565.
ACCESSION AX358167
VERSION AX358167.1 GI:18674876
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SOURCE synthetic construct.
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artificial sequences.
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AUTHORS Fatty acid elongase 3-ketoacyl coa synthase polypeptides
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Db 1183 AGAGCCGTCGATTGATGCTAGAGAAAGAACCTAGCCCTAGCACCGATCGATAGAGGCA 1242
QY 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTrpTyrGluLeu 360
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QY 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
Db 1363 GGTCAAGCTTTAAGTGTAAACAGTGCAGTTTGGTGGCTCTAAACAATGTCAAGGCTCG 1422
QY 401 ThrAsnSerProTyrGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAATATGCTCTGGGAACACTGCATGCACAGATACCCGGTCAAAATGATCTGATTCA 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAACTCAGACTCGTGTGTCAAAACGGTCCGCTCC 1518
RESULT 3
LOCUS AX358169 1521 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 13 from Patent WO0194565.
ACCESSION AX358169
VERSION AX358169.1 GI:18674878
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaworski,J.G. and Blacklock,B.J.
TITLE Fatty acid elongase 3-ketoacyl coa synthase polypeptides
JOURNAL Patent: WO 0194565-A 13 13-DEC-2001;
MIAMI UNIVERSITY (US).


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BASE COUNT 414 a 341 c 343 g 423 t
ORIGIN

Alignment Scores:
Pred. No.: 1.7e-197 Length: 1521
Score: 2238.00 Matches: 430
Percent Similarity: 99.54% Conservative: 0
Best Local Similarity: 99.54% Mismatches: 2
Query Match: 99.25% Indels: 0
DB: 6 Gaps: 0

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QY 21 ValSerLysValMetAspLeuPheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
DQ 283 GTCTCTAAAGTCATGATATTTCTACCAATATAGAAAGCTGATACTTCTTACCGGAC 342
QY 41 GlyThrCysAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
DQ 343 GCGACGCTGATGATTCGTCGGCTTGACTTCTTGAGGAAGATTCACGAAGCTTCAGGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
DQ 403 CTAGCGGATGAACCTCACGGCCCGGCGGCTGCTTCAAGTCCCTCCCGGAGACTTTT 462
QY 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
DQ 463 GCGCGCGCGCGCTGAAGACAGCGGCAAGTATCATTTGTCGCTAGAAAAATCTATTCAAG 522
QY 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
DQ 523 AACACCAACGTTAACCTTAAGATATAGTATACTTGTGTGAACCTCAAGCATGTTTAA 582
QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
DQ 583 CCAACTCCATCGCTCTCCGCGATGCTGCTTAACACTTTCAGCTCCGGAAGCAACGTAAGA 642
QY 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
DQ 643 AGCTTTAACCTTGGTGCGATGGTGTAGTCCGCGGCTTATAGCCATGATCTACCAAG 702
QY 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
DQ 703 GACTTGTGTGATGCTCCATAAAATACGATATGCTTGTGTGTGACGACAGAACATCACT 762
QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
DQ 763 TATACATTTACGCTGGTATATAGTCCATGATGCTGCTTCAATTCCTTGTTCCTGGTT 822
QY 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
DQ 823 GGTGGGCGCGTATTTTGTCTCTCAACAGCGCTGGAGATCGTACGCGGTCCAAGTACGAG 882
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DQ 943 CAAGGAGACGATGAGAACGGCAAAATCGGAGTGAGTTTGTCTCCAGGACATAACCGATGTT 1002
QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
DQ 1003 GCTGGTTCGAACCGTTTAAAGAAACATAGCAACGCTGGGTCCGCTTGTATCTTCCTGTAAGC 1062
QY 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
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QY 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
DQ 1183 AGAGCGGTGATTGATGCTGCTAGAGAAGAACCTAGCCCTAGCACCGATCGATGTAGAGGCA 1242
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DQ 1243 TCAGATCAACGTTACATAGATTGGAACACTTCATCTAGCTCAATATGATGAGTTG 1302
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DQ 1363 GGTTCAGGCTTTAAGTGTACAGTGCAGTTTGGTGGCTCTTAACAATGTCAAAGCTTCG 1422
QY 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
DQ 1423 ACAATAGTCTTGGGAACACTGCTGCACAGATACCGGTCAAAATTTGATCTGTATCA 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
DQ 1483 GGTAACTCAGACACTCGTGTCCAAACGGTCCGCTCC 1518

RESULT 5
AX358171 1521 bp DNA linear PAT 13-FEB-2002
LOCUS Sequence 15 from Patent WO0194565.
DEFINITION AX358171
ACCESSION AX358171
VERSION AX358171.1 GI:18674880
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaworski,J.G. and Blacklock,B.J.
TITLE Fatty acid elongase 3-ketoacyl coa synthase polypeptides
JOURNAL Patent: WO 0194565-A 15 13-DEC-2001;
MIAMI UNIVERSITY (US)
FEATURES
Location/Qualifiers
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hypothetical"
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BASE COUNT 415 a 341 c 342 g 423 t
ORIGIN

Alignment Scores:
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Score: 2235.00 Matches: 429
Percent Similarity: 99.54% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.11% Indels: 0
DB: 6 Gaps: 0

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Qy	21	ValSerLysValMetAspLlePheTyrGlnLleArgLysAlaAspThrSerSerArgAsn	40
Db	283	GYCTCTTAAGTCATGGGATATTTCTACCAATTAAGAAAGCTGATCTCTTCACCGGAAC	342
Qy	41	GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysLleGlnGluArgSerGly	60
Db	343	GGCAGCTGTGATGATCGCTCGTGGCTGACTTCTTGAGGAAGATTCGAAGAACGTTTCAGGT	402
Qy	61	LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe	80
Db	403	CTAGCGGATGAACACTACGGGCCCGAGGGCGTTCAGGTCCCTCCCGGAAGACTTTT	462
Qy	81	AlaAlaAlaArgGluGluThrGluGlnValLleLleGlyAlaLeuGluAsnLeuPheLys	100
Db	463	GGCGGGCGCGCTGAAGAGACGAGCAAGTTATCATTTGGTGGCTAGAAAATCTATTCAAG	522
Qy	101	AsnThrAsnValAsnProLysAspLleGlyLleLeuValValAsnSerSerMetPheAsn	120
Db	523	AACACCAAGTTAACCTTAAGATATAGGTATCTGTTGGTGAACCTCAACGATGTTTAAT	582
Qy	121	ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg	140
Db	583	CCAACCTCCATCGCTCCCGGATGGTCTTAACACTTTTCAAGCTCCGAAGCAACGTAAGA	642
Qy	141	SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValLleAlaLleAspLeuAlaLys	160
Db	643	AGCTTTAACCTTGGTGGCATGGGTGTAGTGGCGGCTTATAGCCATGATGATGATGATG	702
Qy	161	AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnLleThr	180
Db	703	GACTTGTGTGCATGTCCTCAATAAATAGCTATGCTCTGTGGTGAGCAGACAGACATCACT	762
Qy	181	TyrAsnLleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal	200
Db	763	TATACATTTACGCTGGTGATATAGTCCATGATGGTTTCAATTCCTTGTTCCTGTTT	822
Qy	201	GlyGlyAlaAlaLleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu	220
Db	823	GGTGGGGCGCGTATTTTGTCTCCACACAGCTGGAGATCGTAGCGGTCCAAGTACGAG	882
Qy	221	LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln	240
Db	883	CTAGTTACACCGTTCCACGCATACCGGAGCTGACGACAGTCTTTCTGTTGGCTGCA	942
Qy	241	GlnGlyAspAspGluAsnGlyLysLleGlyValSerLeuSerLysAspLleThrAspVal	260
Db	943	CAAGGAGACGATGAGAACGCCAAATTCGGAGTGAGTTTGTCCAAAGGACATAACCGATGTT	1002

Qy	261	AlaGlyArgThrValLysLysAsnLleAlaThrLeuGlyProLeuLleLeuProLeuSer	280
Db	1003	GCTGGTCCGAACGGTTAAGAAAAACATACGAACGTTGGTCCGTTGATTCTTCGCTAAGC	1062
Qy	281	GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLys	300
Db	1063	CAGAAACCTCTCTTTTTCGTTACCTTCATCGGCAAGAACTTTTCAAGAGATAAATCAA	1122
Qy	301	HisTyrTyrValProAspPheLysLeuAlaLleAspHisPheCysLleHisAlaGlyCly	320
Db	1123	CATTACTACGTCGCCGATTTCAAACTTGCTATTGACATTTTGTATACATGCCGGAGGC	1182
Qy	321	ArgAlaValLleAspValLeuGluLysAsnLeuAlaLeuAlaProLleAspValGluAla	340
Db	1183	AGAGCCGCTGATTGATGCTGCTAGAGAAGAACCTAGCCCTAGCACCGATCGATGAGGCA	1242
Qy	341	SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTrpTyrGluLeu	360
Db	1243	TCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGCTATGAGTTG	1302
Qy	361	AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnLleAlaLeu	380
Db	1303	GCATACATAGAAGCAAAAGGAGGATGAAGAAAGTAATAAAGTTGGCAGATTGCTTTA	1362
Qy	381	GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer	400
Db	1363	GGGTACGGCTTTAAGTGTAAACAGTGCAGTTGGTGGCTCTAAACAATGTCMAAGCTTCG	1422
Qy	401	ThrAsnSerProTrpGluHisCysLleAspArgTyrProValLysLysLysAspSer	420
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Qy	421	GlyLysSerGluThrArgValGlnAsnGlyArgSer	432
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RESULT 6

AX358163

LOCUS

DEFINITION

SEQUENCE 7 FROM PATENT WO0194565.

ACCESSION

AX358163.1

VERSION

AX358163.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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1. .1521

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designated At114"

1. .1521

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BASE COUNT 413 a 342 c 342 g 423 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 6,11e-197 Length: 1521
Score: 2232.00 Matches: 428
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Best Local Similarity: 99.07% Mismatches: 3
Query Match: 99.98% Indels: 0
DB: 6 Gaps: 0

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QY 21 ValSerLysValMetAspLysPheTyrGlnLeuArgLysAlaAspThrSerSerArgAsn 40
DB 283 GTCTCTAAGTCATGGATATTTCTACCAAAATAGAAAGCTGATCTTCTTCACGGAAC 342
QY 41 GlyThrCysAspSerSerTyrLeuAspPheLeuArgLysLysLysLysLysLysLys 60
DB 343 GGCACGTGTGATGATTCGTGCGTGTGACTTCTTGAGGAAGATTCAGAACGTTTCAGGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
DB 403 CTAGCGGATGAATCTACGGCCGCGAGGGCGTCTTCAGGTCCCTCCCGGAAGACTTTT 462
QY 81 AlaAlaAlaArgGluThrGluGlnValLysLysLysLysLysLysLysLysLysLys 100
DB 463 CGCGCGCGCGCGTGAAGAGACGAGCAAGTATCATTTGGTGGCTAGAAAATCTATTCAG 522
QY 101 AsnThrAsnValAsnProLysAspLysLysLysLysLysLysLysLysLysLys 120
DB 523 AACACCAACGTTAACCTTAAGATATAGTACTTGTGGTGAACCAAGCATGTTTAAAT 582
QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
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QY 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValLysLysLysLysLysLys 160
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QY 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnLys 180
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QY 181 TyrAsnLysTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
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QY 201 GlyGlyAlaAlaLysLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
DB 823 GGTGGGGCCGCTATTTTGTCTCCAAACAGCCTCGAATCTAGACGGTCCAAAGTACGAG 882
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DB 1483 GGTAACTGAGAGACTCGTGTCCCAACGCGTGGTCC 1518
RESULT 7
AX358165 AX358165 1518 bp DNA linear PAT 13-FEB-2002
LOCUS Sequence 9 from Patent WO0194565.
DEFINITION AX358165
ACCESSION AX358165
VERSION AX358165.1 GI:18674874
KEYWORDS
SOURCE .
ORGANISM synthetic construct.
REFERENCE synthetic construct
1 artificial sequences.
Jaworski, J. G. and Blacklock, B. J.
TITLE Fatty acid elongase 3-ketoacyl coA synthase polypeptides
JOURNAL Patent: WO 0194565-A 9 13-DEC-2001;
MIAMI UNIVERSITY (US)
FEATURES
location/Qualifiers
source
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designated At74"
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BASE COUNT 415 a 343 c 344 g 416 t
ORIGIN

Alignment Scores:
Pred. No.: 9.1e-195 Length: 1518
Score: 2208.50 Matches: 424
Percent Similarity: 99.07% Conservativity: 3
Best Local Similarity: 98.38% Mismatches: 3

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Query Match: 97.94% Indels: 1
DB: 6 Gaps: 1
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Qy 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
Db 286 TCCAGGTCATGATATCTTTATCAAGTAAGAAAGCTGAT---CCTTCTCGAAGCGC 342
Qy 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
Db 343 ACGTGGGATGACTCGCTGGCTTGACTTCTTGAGAGAGATTCAGAACGCTTCAGGTCTA 402
Qy 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
Db 403 GGGGATGAACCTACGGCCCGAGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTTCG 462
Qy 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
Db 463 CGCGCCGCGAAGACCGAGCAAGATTATCATTTGGTGGCTAGAAAATCTATTCAAGAAC 522
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Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
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Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401
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Db 1483 AAGTCAGAGACTCGTGTCCAAAACGTCGGTCC 1515

RESULT 8
LOCUS AX358159 1524 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 3 from Patent WO0194565.
ACCESSION AX358159
VERSION AX358159.1 GI:18674868
KEYWORDS
SOURCE rape.
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS Jaworski, J.G. and Blacklock, B.J.
TITLE Fatty acid elongase 3-ketoacyl coA synthase polypeptides
JOURNAL Patent: WO 0194565-A 3 13-DEC-2001;
MIAMI UNIVERSITY (US)
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BASE COUNT 421 a 350 c 344 g 409 t
ORIGIN

Alignment Scores:
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Score: 2208.50 Matches: 424
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Best Local Similarity: 98.38% Mismatches: 3
Query Match: 97.94% Indels: 1
DB: 6 Gaps: 1

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Qy 62 GlyAspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAla 81
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Qy 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
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Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
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Db 1486 AAGTCAGAGACTCGTGTCCAAAACGGTTCGGTCC 1518

RESULT 9
AF009563
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica napus.
Brassica napus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 1525)
AUTHORS
Clemens, S. and Kunst, L.
TITLE
Isolation of a Brassica napus cDNA (Accession No. AF009563)
encoding 3-ketoacyl-CoA synthase, a condensing enzyme involved in
the biosynthesis of very long chain fatty acids in seeds
(JG897-125)
JOURNAL
Plant Physiol. 115, 313-314 (1997)
REFERENCE
2 (bases 1 to 1525)
AUTHORS
Clemens, S. and Kunst, L.
TITLE
Direct Submission
JOURNAL
Submitted (19-JUN-1997) Botany, University of British Columbia,
6270 University Blvd., Vancouver, BC V6T 1Z4, Canada
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BASE COUNT 422 a 350 c 344 g 409 t
ORIGIN

Alignment Scores:
Pred. No.: 9,16e-195 Length: 1525
Score: 2208.50 Matches: 424
Percent Similarity: 99.07% Conservative: 3
Best Local Similarity: 98.38% Mismatches: 3
Query Match: 97.94% Indels: 1
DB: 8 Gaps: 1

SEQ12-JOIN-SBQ4 (1-432) x AF009563 (1-1525)
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Db 289 TCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGAT---CCTTCTCGGAACGGC 345
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Db 346 ACGTGGATGACTCGCTGGCTTGACTCTTGAGGAGATTCAGAACCGTTCAGTCTCA 405
QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
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LOCUS AX358173
DEFINITION Sequence 17 from Patent WO0194565.
ACCESSION AX358173
VERSION AX358173.1 GI:18674882
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaworski, J.G. and Blacklock, B.J.
TITLE Fatty acid elongase 3-ketoacyl coa synthase polypeptides
JOURNAL Patent: WO 0194565-A 17 13-DEC-2001;
MIAMI UNIVERSITY (US)
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ORIGIN

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Best Local Similarity: 98.14% Mismatches: 4
Query Match: 97.63% Indels: 1
DB: 6 Gaps: 1

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QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTrpGluLeu 221
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QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
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RESULT 11
AX358189
LOCUS AX358189
DEFINITION Sequence 33 from Patent WO0194565.
ACCESSION AX358189
VERSION AX358189.1 GI:18674898
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE
1 Jaworski, J.G. and Blacklock, B.J.
Fatty acid elongase 3-ketoacyl coa synthase polypeptides
Patent: WO 0194565-A 33 13-DEC-2001;
MIAMI UNIVERSITY (US)
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Pred. No.: 4,07e-194 Length: 1524
Score: 2201.50 Matches: 423
Percent Similarity: 98.84% Conservative: 3
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 97.63% Indels: 1
DB: 6 Gaps: 1
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QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
Db 346 ACCTGGGATGACTCGCTCGCTGGCTTGAATCTTGTGAGAGAGATTCAAGAACGTTTCAAGTCTA 405
QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
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Qy 142 PheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
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Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 886 GTTCACACGGTTCGAAGCATACCGGAGCTGACGACAACTCTTTCGTTGGTGCACAA 945
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Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
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DEFINITION Sequence 17 from Patent WO02052024.
ACCESSION AX473307
VERSION AX473307.1 GI:22207959
KEYWORDS
SOURCE
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
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AUTHORS Willmer,J.A. and Wallington,E.J.
TITLE Elongase promoters
JOURNAL Patent: WO 02052024-A 17 04-JUL-2002;
BIOSIS Previews
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BASE COUNT 423 a 350 c 342 g 409 t
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Pred. No.: 4,07e-194 Length: 1524
Score: 2201.50 Matches: 423
Percent Similarity: 98.84% Conservative: 3
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 97.63% Indels: 1
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DEFINITION Sequence 17 from Patent WO0111061.
ACCESSION AX083739
VERSION AX083739.1 GI:13185467
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 1588)
AUTHORS Kunst, L. and Clemens, S.
TITLE Regulation of embryonic transcription in plants
JOURNAL Patent: WO 011061-A 17 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
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Pred. No.: 4,3e-194 Length: 1588
Score: 2201.50 Matches: 423
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Best Local Similarity: 98.14% Mismatches: 4
Query Match: 97.63% Indels: 1
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QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
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DEFINITION Brassica napus beta-ketoacyl-CoA synthase (FAE1.1) mRNA, complete cds.
ACCESSION AF274750
VERSION AF274750.1 GI:14495234
KEYWORDS
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ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Han,J., Luhs,W., Sonntag,K., Zahringner,U., Borchardt,D.S., Wolter,F.P., Heinz,E. and Frentzen,M.
TITLE Functional characterization of beta-ketoacyl-CoA synthase genes from Brassica napus L.
JOURNAL Plant Mol. Biol. 46 (2), 229-239 (2001)
MEDLINE 21335051
PUBMED 11442062
REFERENCE 2 (bases 1 to 1704)
AUTHORS Han,J., Wolter,F.P. and Frentzen,M.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-2000) Institute of General Botany, University of Hamburg, Ohthorststr. 18, Hamburg, Hamburg 22609, Germany
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BASE COUNT 478 a 368 c 371 g 487 t
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Alignment Scores:
Pred. No.: 4,75e-194 Length: 1704
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Percent Similarity: 98.84% Conservative: 3
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 97.63% Indels: 1
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QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
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DEFINITION Sequence 1 from Patent WO0129238.
ACCESSION AX1271154
VERSION AX1271154.1 GI:14041154
KEYWORDS
SOURCE
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 1785)
Wolter,F.P., Han,J. and Frentzen,M.
Elongase promoters for the tissue-specific expression of transgenes
in plants
Patent: WO 0129238-A 1 26-APR-2001;
GVS Gesellschaft fuer Erwerb und Verwertung von Schutzrechten MBH
(DE)
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/db_xref="taxon:3708"
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Score: 2201.50 Matches: 423
Percent Similarity: 98.84% Conservative: 3
Best Local Similarity: 98.14% Mismatches: 4
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Qy 402 AsnSerProTyrGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
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 Db 1507 AATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAAATTGATTCTGATTCAGGT 1566

Qy 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
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 Db 1567 AGTCAGAGACTCGTGTCCAAAACGGTCGGTCC 1599

Search completed: January 6, 2003, 18:09:58
 Job time : 2441 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: January 6, 2003, 16:31:35 : Search time 39 Seconds
(without alignments)
3397.035 Million cell updates/sec

Title: SEQ12-JOIN-SEQ4

Perfect score: 2255

Sequence: 1 NPVILVDYSCVLPHPHCRVS.....PVKIDSDSGKSETRVQNGRS 432

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2010	89.1	1641	4	US-09-362-633-1 Sequence 1, Appli
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4	1503.5	66.0	1548	4	US-08-868-373-13 Sequence 13, Appli
5	1487.5	66.0	1479	4	US-08-868-373-3 Sequence 3, Appli
6	1473.5	65.3	1512	4	US-08-868-373-5 Sequence 5, Appli
7	1277.5	56.7	1783	1	US-08-066-299-11 Sequence 11, Appli
8	1277.5	56.7	1783	1	US-08-265-047-3 Sequence 3, Appli
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10	1259.5	55.9	1502	4	US-08-868-373-11 Sequence 11, Appli
11	1259.5	55.9	1807	4	US-09-058-947A-2 Sequence 2, Appli
12	1259.5	55.9	3722	4	US-09-058-947A-1 Sequence 1, Appli

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15	1258	55.8	1733	4	US-08-926-522-21 Sequence 21, Appli
16	1241.5	55.1	1560	4	US-08-868-373-1 Sequence 1, Appli
17	1119	49.6	1650	4	US-08-868-373-7 Sequence 7, Appli
18	625.5	27.7	383	3	US-08-888-998-3 Sequence 3, Appli
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22	186	8.2	5076	2	US-08-494-907-2 Sequence 2, Appli
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24	186	8.2	6170	2	US-08-494-907-4 Sequence 4, Appli
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27	186	8.2	6387	5	PCT-US96-10986-3 Sequence 3, Appli
28	181.5	8.0	1047	2	US-08-494-907-11 Sequence 11, Appli
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30	181.5	8.0	3680	2	US-08-494-907-1 Sequence 1, Appli
31	181.5	8.0	3680	5	PCT-US96-10986-1 Sequence 1, Appli
32	164.5	7.3	2728	3	US-08-836-402B-7 Sequence 7, Appli
33	156	6.9	1359	4	US-09-252-816A-2 Sequence 2, Appli
34	155.5	6.9	747	5	PCT-US91-06234A-6 Sequence 6, Appli
35	152	6.7	23673	4	US-09-773-816-1 Sequence 1, Appli
36	131	5.8	1485	1	US-08-471-601-23 Sequence 23, Appli
37	131	5.8	1485	1	US-08-474-556-23 Sequence 23, Appli
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40	131	5.8	1485	1	US-08-479-383-23 Sequence 23, Appli
41	131	5.8	1485	2	US-08-479-041-23 Sequence 23, Appli
42	131	5.8	1485	4	US-08-819-646-23 Sequence 23, Appli
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ALIGNMENTS

RESULT 1
US-08-888-998-1
; Sequence 1, Application US/08888998
; Patent No. 6124524
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAEL GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,998
; FILING DATE: 07-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,603
; FILING DATE: 26-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 12176-004300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600

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; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1641 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: both
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: 1..1641
;   OTHER INFORMATION: /product= "FAE1 from Arabidopsis"
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; US-08-888-998-1
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Db 343 GTGGCATGTGATGATCGCTCGCTCGATTTCTCGAGAGATTCAGAGCGTTT 402
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGGTGATGAGACGTACAGCTCTGAGGAGCTCATTCAGCTACCCACCGCGAAGACTTTT 462
Qy 81 AlaAlaAlaArgGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCAGCGTCACGTGAGAGACAGAGAGAGTTATCATCGTGGCTCGCAAAATCTATTTCGAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
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Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCTCTCGCTATCCGCTATGGTCTGTTAATCTTCAAGCTCCCAAGTCAACATCAA 642
Qy 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
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Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
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Qy 401 ThrAsnSerProTrpGluHisCysLysLeuAspArgTyrProValLysLysSerAspSer 420
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US-09-362-633-1
; Sequence 1, Application US/09362633
; Patent No. 6184355
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAE1 GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,633
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,998
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 12176-004300
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Qy 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
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Qy 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLys 282
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Db 1207 ATTCTGTTTTCATGACTTGGTTTACGAAGAACTGTTTAACTCCAAGCTCAAGCGC--- 1263
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RESULT 4

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; Sequence 13, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beittemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868.373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-13
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Score: 1503.50 Matches: 284
Percent Similarity: 81.45% Conservative: 54
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Query Match: 66.67% Indels: 11
DB: Gaps: 3
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Db 391 GCTCGGTTTCATG-----GAACATTTCTAGACTCACCGGA 423
Qy 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
Db 424 GATTTCGATGACTCTGCT---CTCGAGTTTCACGCAAGATCCTTGAGGCTTCTGTTA 480
Qy 62 GlyAspGluThrHisGlyProGluGlyLeuGluValProProArgLysThrPheAla 81
Db 481 GGGGAAGACACTTATGCTCCTGAACTATGCTATGCTTCCACCGAGAATTTCAATGGCT 540
Qy 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
Db 541 GCTGCTAGAGAAGAAGCTGAACAAGTCATGTTGGTCTTTAGATAACCTTTCCCTAAC 600
Qy 102 ThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnPro 121
Db 601 ACTAATGTGAACAACAAGATATGGAATCTCTTGTGTAATTTGTAGTCTCTTTAATCCA 660
Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
Db 661 ACTCCTTCGTTATCTGCAATGATTGTGAACAAGTATAAGCTTAGAGGTAAACATTAGAGC 720
Qy 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db 721 TACAATCTAGCGGTATGGTTGTCAGCGCGGAGTTATCGCTGGATCTTGTCTTAAGAC 780
Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
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Db 781 ATGTTGTTGGTACATAGGAACACTTATGCGGTTGTTGTTTCTACTGAGAACATTACTCAG 840
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Db 841 AATTGGTATTGGTACAGAAATCGATGTTGATCCGAACCTGCTGTTTCGAGTGTG 900
Qy 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 901 GGCTCTGGGGTTTTCGTATCGAACAAAGTCGAGGACAAAGACGCGTCTAAGTACAGGCTT 960
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Db 961 GTACATGTAGTCAGGACTCACCGTCGAGCAGATGATAAGCTTTCCTGTTGTTTATCAA 1020
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db 1021 GAGCAGGATGATACAGGAGAAACCGGGTTTCGTTGTCGAAGATCTTAATGGCGATTGCA 1080
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
Db 1081 GGGAAACTCTCAAAACCATATCACTACATTGGCTCTCTGTTCTACCGATAAGTGAG 1140
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
Db 1141 CAGATCTCTCTTTATGACTCTAGTTGTGAAGAAGCTCTTTAAACGGTAAAGTGAACCG 1200
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
Db 1201 ---TATATCCGGATTCNAACCTTGCTTCGAGCATTTCTGTATCCATGCTGGTGGAGA 1257
Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db 1258 GCTGTGTCGATGATGATAGAGAAGATCTGCAGCTTTCACCAAGTTCATGTCGAGGCTCG 1317
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrGlyGluLeuAla 361
Db 1318 AGGATGACTCTTCATCGATTGTTGTAACACATCTTCGACCTCCATTTGGTATGANTGGCT 1377
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
Db 1378 TCATTTGAAGCGAAGGAGGATGCGAAGAGTAAATCGTTTGGCAAAATCGCGTTTCGGA 1437
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401
Db 1438 AGTGATTTAAATGATTAATGCGCGATTTCGGGAAGCATTAAGGCATGTGAACCTTCGAC 1497
Qy 402 AsnSerProTyrGluHisCysIleAspArgTyrProValLysIle 416
Db 1498 AACAGTCTTGGGAAGATTTGATTGACAAGTATCCGGTAACCTTTA 1542

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RESULT 5

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US-08-868-373-3
; Sequence 3, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltenham, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-3

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Alignment Scores:

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Pred. No.: 1,37e-164 Length: 1479
Score: 1487.50 Matches: 281

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Percent Similarity: 81.38% Conservative: 60
Best Local Similarity: 67.08% Mismatches: 71
Query Match: 65.96% Indels: 7
DB: 4 Gaps: 3

SEQ12-JOIN-SEQ4 (1-432) x US-08-868-373-3 (1-1479)

Qy 2 ProValTyrLeuValAspTyrSerCystTyrLeuProProHisCysArgValSerVal 21
Db 232 CCCGTTTATCTCGCTGACCTTTAGCTGTACTCCACCCTCGCATCTCAAGCCAGCAC 291
Qy 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
Db 292 CAGAGGATCATCAACACGTAAGGCTTGTAGAGAAGCAGGCGCTGGAAGCAA----- 345
Qy 42 ThrCysAspAspSerSerTyrLeu---AspPheLeuArgLysIleGlnIleArgSerGly 60
Db 346 -----GAGTCCGATTACTTGATGACCTTCGCGAGAAGATTCTAGAAGTTCGCGT 396
Qy 61 LeuGlyAspGluThrHisGlyProGlyLeuLeuGlnValProArgLysThrPhe 80
Db 397 CTAGGCCAAGAGACGTACTACCCGGAAGGCTTTCAAACTTTTGCCACTACACAGAAATTTG 456
Qy 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 457 GCTCTATCATCGTATACAGACGCGAGGAAGTATTATTGTCGCGTCAATCTGTTTCGC 516
Qy 101 AsnThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsn 120
Db 517 AACACGGGAATAGCCCTAGTATAGTATATGTTGTTGTAATTTCAAGCACTTTTAAAT 576
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 577 CCAACACCTTCGCTATCAAGTATCTTAGTGAATAAGTTTAACTTAGGATATAATAAAG 636
Qy 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 637 AGCTTGTAATCTTGGTGGGATGGGTGTAGCGCTGGAGTCACTGCTATCGATCGCGCTAAG 696
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 697 AGCTTGTTTACAACTTCATAGAAACACTTATGCTCTTGTGTCGAGCAGCGAGAATCACT 756
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 757 CAABAACCTTGATACATGGGTAAACAAATCAATGTTGTTTACAAACTGTTTGTTCGATA 816
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 817 GGTGGGCGCGGATTTTGTCTTAAACCGTCTATAGATCGTAAACGCGCAAAATACGAG 876
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 877 CTTGTTCCACCGCTGGGTCCATACCGGACGATGACCGATCTTATGATGATGTCGAAC 936
Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 937 CAAGAAGAGGATGAAGATGGCATAGTGGGTTCCTTGTTCGAAGAATCTACCAATGTA 996
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 997 GCTCCAAGAACCCTAAAGATCAATATCGAACTTTGGTCCGCTGTTTCTTCCCAATAGC 1056
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
Db 1057 GAGAAGTTTCACTTCTTGTGAGGTTCTGTTTAAAAAAGAGTTTCTCAACCCCAAGCTAAG 1116
Qy 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyCly 320
Db 1117 CAT---TACATTCCGATTTCAAGCTCGCATTCGATTCGATTCATCATCGCGGTGGT 1173
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340

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Db	625	ACTCCATCACTCGCCTCCATGATGTGTGAACAAGTACAACATTCAGACAGACAACATCAAGAGT	684
Qy	142	PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp	161
Db	685	TTGAATCTTGGAGGANTGGGTTCAGTCCGGAGTTATACCTGTTGATGTCGTAAAGGA	744
Qy	162	LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr	181
Db	745	TTACACAAAGTTTCATAGGAACACTTATGCTATTTGTTAGTAAAGACAGACAACATCACTCAG	804
Qy	182	AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly	201
Db	805	ACITATATCTTGGGNAACAAATCAATGCTAGTCACAACTGTTGTTCCGGTTGGT	864
Qy	202	GlyAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu	221
Db	865	GGTGCTCGGTTCTGCTTTCAACACAGACTAGACACCGTAAACGGCCGCAATACGAGCT	924
Qy	222	ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln	241
Db	925	GTTACACACCGTACGGATCATACCGGATCAGATGATAGGTCGTTGCAATGTCGCACACA	984
Qy	242	GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla	261
Db	985	GAAGAGATGAGATGGTATTAATTTGAGTTTCCTTGCACAAAGAACTTACCTATGTTGGT	1044
Qy	262	GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu	281
Db	1045	GCAAGGACTCTTAAGATAAATATCGCAACTTTGGGTCTCTTGCTACTCCATTTAAAGAG	1104
Qy	282	LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis	301
Db	1105	AAGCTAGCCTTCCTTATATCTTTGTCAGAGAAGATATTTCAAGCCAGAGCTTAAGGAAT	1164
Qy	302	TyrTyrValProAspPheLysLeuAlaIleAspPheLysPheCysIleHisAlaGlyGlyArg	321
Db	1165	--TATACACAGATTTCACGCTTGCTTGGCATTTCTGTATCCACGCTGTTGGAAGA	1221
Qy	322	AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer	341
Db	1222	GCTCTATATAGTACGCTGGAGAGACCTTAGCTTCTCGGTTACAGTAGAGCGCTCA	1281
Qy	342	ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTyrTyrGluLeuAla	361
Db	1282	AGAAATGACACTACACAGGTTTGGTAAACATCTTCTAGCTCAATCTGGTAGGATAGCT	1341
Qy	362	TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly	381
Db	1342	TATACAGACCTTAAGGAAGGATGAGGAAGGAGATAGGATTTGGCAGNATGCTTTGGGG	1401
Qy	382	SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr	401
Db	1402	TCAGGTTTTAAGTGTAAACAGTTTCAGTATGGGTGGCTCTCGGAGACGCTTAAGSCCTCAGCT	1461
Qy	402	AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAsp	417
Db	1462	ACAGTCCATGGGACACACTGTATGGATAGATATCGGTTGAGATTGAT	1509

RESULT 7

us-08-066-299-11

; Sequence 11, Application us/08066299

; Patent No. 5445947

; GENERAL INFORMATION:

; APPLICANT: James George Metz

; APPLICANT: Kathryn Dennis Lardizabal

; APPLICANT: Michael W. Lassar

; TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol

; TITLE OF INVENTION: O-Acyltransferases

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Calgene, Inc.

; STREET: 1920 Fifth Street

CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 6.0.7
 SOFTWARE: Microsoft Word 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/066,299
 FILING DATE: 19930520
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/796,256
 FILING DATE: 20-NOVEMBER-1991
 APPLICATION NUMBER: 07/933,411
 FILING DATE: 21-AUGUST-1992
 APPLICATION NUMBER: PCT/US92/09863
 FILING DATE: 13-NOVEMBER-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 REFERENCE/DOCKET NUMBER: CGNE 98
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-066-299-11

Alignment Scores:

Pred. No.: 7,69e-140 Length: 1783
 Score: 1277.50 Matches: 245
 Percent Similarity: 75.42% Conservative: 68
 Best Local Similarity: 59.04% Mismatches: 91
 Query Match: 56.65% Indels: 11
 DB: 1 Gaps: 3

SEQ12-JOIN-SEQ4 (1-432) x US-08-066-299-11 (1-1783)

QY 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerValSer 22
 DB 334 GTCTACTTGTGGAGTCTTGGCTCTAAGCCTCACCAGAACCTGATAACATCCACGAG 393
 QY 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
 DB 394 ATGTTTCATG-----GACCGGACCTCCCGGCGCGGTGCG 426
 QY 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnArgSerGlyLeuGly 62
 DB 427 TTTTCTAAGGAGAAT---ATTGAGTTTCAGAGGAAGATCTTGGAGAGGCGCGGTATGGCG 483
 QY 63 AspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAlaAla 82
 DB 484 CGGGAACCTACGTCCTCCGAATCCGTCACCTAAGTGGCGCGCGGCGGAGCATAGCAGCA 543
 QY 83 AlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThr 102
 DB 544 GCAGGGCGGAGGCGGAGGAGGTGATGTCAGGGCGGATCGACGAGGTGTGGAGAAGACG 603
 QY 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122
 DB 604 GGGGTGAAGCGAGCAGATAGGACTGTTGGTGGTGAACCTGTTTACCCACG 663
 QY 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142

DB 664 CCGTCGCTGTCATCCATGATAGTTAACCATTTACAGCTTAGGGGTAATATCTAGCTAT 723
 QY 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162
 DB 724 AATCTTGTGGCATGGTTGCAGTCTGGGCTCATTTCCATTGATCTTGCCAAAGACCTC 783
 QY 163 LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsn 182
 DB 784 CTACAGGTTTACCGTAACACATATGTGTAGTAGCAGACACAAACATGACCTTAAT 843
 QY 183 IleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGly 202
 DB 844 TGGTACTGGGGCAATGACGCTCCATGCTTATACCAACTGCTATTTCGATGGGTGGC 903
 QY 203 AlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrCluLeuVal 222
 DB 904 GCTGCCATCATCTCTCAAAACCGTGGCGGTGTCGCGCATCCAAAGTACCACTCTT 963
 QY 223 HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGly 242
 DB 964 CACACAGTAGCCACCCACCAAGGGCGCTGACGACAAAGTCTTATAGATGCGCTTCAACA 1023
 QY 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
 DB 1024 GAAGTCAAAATAACAAAGTAGGTGTGCTTATCCAAAGATCTGATGCGAGTGGCGGT 1083
 QY 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSerGlyLys 282
 DB 1084 GAAGCCCTAAAGGCCAACATCAGACCCCTTGGTCCCTGCTGCCATGTCAGAACAA 1143
 QY 283 LeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyr 302
 DB 1144 CTCCTCTCTTCCACCTTAGTGGCAGCTAAGGTCTTCAAGATGACGACGACGAGCCCA 1203
 QY 303 TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyIleArgAla 322
 DB 1204 TACATCCAGATTCAAGTTGGCAGCAACTTCTGTGATCATCGAGGAGGCAAGCA 1263
 QY 323 ValIleAspValLeuGlyLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342
 DB 1264 GTGTGGATGAGCTCGAGAGCACTTGGAGTTGACGCCATGGCCCTTGACCCCTCGAGG 1323
 QY 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTrpTrpGluLeuAlaTyr 362
 DB 1324 ATGACACTGTATAGTTTGGGAACACATCGAGTAGCTCATTTATGTTAGGTTGGCATAC 1383
 QY 363 IleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGlySer 382
 DB 1384 GCTGAAGCAAAAGGGAGGATCGTAAGGGTATCGAACCTTGATGATGGATTGGTTCA 1443
 QY 383 GlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLys---AlaSerThr 401
 DB 1444 GGTTCAGGTGAACAGTGTGTGTGGAGGCTTGGAGGAGTGTCAATCCGCGCTAGAGAG 1503
 QY 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIle 416
 DB 1504 AAGAACTCTTGGATGATGAAATTGAGAAATTTCCCTGTCCATGTG 1548

RESULT 8

US-08-255-047-3

; Sequence 3, Application US/08265047

; Patent No. 5679881

; GENERAL INFORMATION:

; APPLICANT: Metz, James G.

; APPLICANT: Lardizabal, Kathryn D.

; APPLICANT: Lasser, Michael

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding a Plant Cytoplasmic Protei

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESS: Calgene, Inc.

; STREET: 1920 Fifth Street

; CITY: Davis

```
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,047
; FILING DATE: 23-JUN-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/160,602
; FILING DATE: 30-NOV-93
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/796,256
; FILING DATE: 20-NOV-91
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/933,411
; FILING DATE: 21-AUG-92
; APPLICATION NUMBER: 08/066,299
; FILING DATE: 20-MAY-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09863
; FILING DATE: 13-NOV-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 101-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 3 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; US-08-265-047-3

Alignment Scores:
Pred. No.: 7,69e-140 Length: 1783
Score: 1277.50 Matches: 245
Percent Similarity: 75.42% Conservative: 68
Best Local Similarity: 59.04% Mismatches: 91
Query Match: 56.65% Indels: 11
DB: 1 Gaps: 3

SEQ12-JOIN-SEQ4 (1-432) x US-08-265-047-3 (1-1783)

QY 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerValSer 22
Db 334 GTTCTTGTGGATCTTTGGCTGCTATACCTCACCCGACCTGATACATACATCCAGG 393
QY 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsnGlyThr 42
Db 394 ATGTTTCATG-----GACCGGACCTCCCGGGCGGGTGC 426
QY 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeuGly 62
Db 427 TTTTCTAAGGAGAAAT---ATTGAGTTTCAGAGGAGAAATCTTGAGAGGGCCGGTATGGCC 483
QY 63 AspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAlaAla 82
Db 484 CGGGAACACCTAGCTCCCGAAATCCGTCATTAAGTCCGCCCGGAGCCGAGCATGACGCA 543
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QY 83 AlaArgGluGluThrGluGlnValIleLeuGlyAlaLeuGluAsnLeuPheLysAsnThr 102
Db 544 GCCAGGCGCGAGGCGGAGGAGGTGATGACGGGGCGATGACGAGGTGTGGAGAGACG 603
QY 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122
Db 604 GGGGTGAAGCGGAGGAGATAGTAATCTGGTGGTGAACCTGCAGCTTGTTAACCCACG 663
QY 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
Db 664 CGGTGCTGTATCCATCATAGTTAACCATTACAAAGCTTAGGGGTAAATATAGTACTAT 723
QY 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysLeu 162
Db 724 ATCTTGTGGCATGGGTGCGAGTCTGGGTCTATTTCCATGTATCTTCCAGGACCTC 783
QY 163 LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsn 182
Db 784 CTACAGGTTTACCGTACACATATGTGTAGTAGTACGACACAGAAACATGACCTTAA 843
QY 183 IleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 202
Db 844 TGGTACTGGGGCAATGACCGCTCCATGCTTATCACAACCTGCCTATTTGCGATGGTGGC 903
QY 203 AlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuVal 222
Db 904 GGTGCCATCATCTCTCAACCGCTGGCGTGTGCTGCGCGATCCCAAGTACCAACCTCTT 963
QY 223 HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGly 242
Db 964 CACACAGTACGCAACCCACCAAGGGCGCTGACGACAAAGTCTTATAGATGCGTCTTACAACAA 1023
QY 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
Db 1024 GAAGATGAATAATACAAAGTAGGTGTGCTTATCCAAAGGATCTGATGCGCATGCCCGT 1083
QY 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSerGluLys 282
Db 1084 GAAGCCCTAAAGGCCAACATCACGACCTTGGTCCCTCGTGTGCTCCCATGTCAGAACAA 1143
QY 283 LeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLysHisTyr 302
Db 1144 CTCCTCTCTTTGCCACCTTAGTGGCAGCATGAAGTCTTCAAGATGACGACGAGTGAAGCCA 1203
QY 303 TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAla 322
Db 1204 TACATCCAGATTTCAAGTTGGCAGCGAAGCACTTCTGCATCCATGCAGGAGGCAAGCA 1263
QY 323 ValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342
Db 1264 GTTGTGGATGAGCTCGAGACGAACTTGGAGTTGACGCCATGGCCCTTGAACCCCTCGAGG 1323
QY 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerSerSerSerSerSerSerSer 362
Db 1324 ATGACACTGTATAGTTTGGGAACACATCGAGTAGCTCATTTATGTTACGAGTTGTCATAC 1383
QY 363 IleGluAlaLysGlyArgMetLysLysLysLysLysValTrpGlnIleAlaLeuGlySer 382
Db 1384 GCTGAAGCAAAAGGAGGATCCGTAAGGGTGTATCGAACTTGGATGATGGATTTGGTTCA 1443
QY 383 GlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLys---AlaSerThr 401
Db 1444 GGTTCAGTGTAACTGTTGTGGAGGGCTTGGAGGAGTGTCAATCCGGCTAGAGAG 1503
QY 402 AsnSerProTrpGluHisCysLysAspArgTyrProValLysIle 416
Db 1504 AAGATCTCTGGATGGATGAATTTGAGAATTTCCCTGTCCATGTG 1548
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RESULT 9

US-09-058-947A-3

; Sequence 3, Application US/09058947A

; Patent No. 6274790

! CURRENT FILING DATE: 1997-06-03
! NUMBER OF SEQ ID NOS: 22
! SOFTWARE: FastSeq for Windows Version 3.0
! SEQ ID NO 11
! TYPE: DNA
! ORGANISM: Arabidopsis thaliana
US-08-868-373-11

Alignment Scores:
Pred. No.: 7.57e-138 Length: 1502
Score: 1259.50 Matches: 238
Percent Similarity: 73.67% Conservative: 67
Best Local Similarity: 57.49% Mismatches: 98
Query Match: 55.85% Indels: 11
DB: 4 Gaps: 2

SEQ12-JOIN-SEQ4 (1-432) x US-08-868-373-11 (1-1502)

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Qy 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerValSer 22
Db 274 ATCTACTCGTTCGACATATCTGTGTACAGCCACCTGTCTGTCGTGTCCTCGCA 333
Qy 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
Db 334 ACTTTCATGGACACTCTCGTTGATCTCTCAG----- 366
Qy 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeuGly 62
Db 367 ---GACAGCCCTAAGAGCGGTGCGAGTTCCAAATGAGAACTTGAACGTTCTGCGCTCGGT 423
Qy 63 AspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAlaAla 82
Db 424 GAGGAGACTGTGTCCTCCGCGGTATTCATATATATCTCCACACCAACCTGGAGCGG 483
Qy 83 AlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThr 102
Db 484 GCTTAGAGCGAGGCTCAGATGTTATCTCGAGCGCCATGGAGCATCTTTTCAAGAAACCC 543
Qy 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122
Db 544 GGTCTTAAACCTTAAAGAGCTGCAGATCTTATGTCMACTGCTCTCTTTCTCTCCACA 603
Qy 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
Db 604 CCATCGCTCAGCTATGCTGTCACAAATATAGCTTGAAGTATATATCAAGAGCTTC 663
Qy 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162
Db 664 AATCTTTCCGGGATGGCTGCAGCGCGGCTGATCTCAGTTGATCTAGCCCGACTTG 723
Qy 163 LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsn 182
Db 724 CTCCAAGTTCATCCCAATTCMAATGATCATGTCGACGAGAGATCATACGCTAAT 783
Qy 183 IleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGly 202
Db 784 TACTATCAAGGCAAGCAGAGAGCATGTTGTACCAATTTGCTCTCCGCTGGGTGG 843
Qy 203 AlaAlaLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuVal 222
Db 844 CGAGCCATACATGTCAAACCGCGGTCTGACCGGTGGCGGCAATACAGCTTCC 903
Qy 223 HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGly 242
Db 904 CACCTCGTCGGACACACCGTGGCGGTGACGACAAAGTCTTTCTACTGTGTACGAACAG 963
Qy 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
Db 964 GAAGACAAAGAGGACCGTGGCATCACTGTGTCCAAAGATCTATGCGCCATCGCGGT 1023
Qy 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuProLeuSerGluLys 282
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Db 1024 GNAGCCCTCAAGGCAACATACACCATAGTCTCTTGGTCTACCGCGGTCAAGACAA 1083
Qy 283 LeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyr 302
Db 1084 CTTCTCTCTCTCCTACGTCCTTAATCGAGGTAAATCTTCAACCGGAAATGGAACCA 1140
Qy 303 TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAla 322
Db 1141 TACATACCGGATTCATCAAGTCCGCTTCGAACACTTTTGCATTCACGAGGAGAGCG 1200
Qy 323 ValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342
Db 1201 GTGATCGACGAGCTCCAAAGAAATCTCAACATATCAGGAGAACACACGTTGAGGCTCAAGA 1260
Qy 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrTyrGluLeuAlaTyr 362
Db 1261 ATGACACTACATCGTTTGGTAAACAGCTCATCTTCATCTGTTATGTTACGAGCTTAGCTTAC 1320
Qy 363 IleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGlySer 382
Db 1321 ATCGAGTCTTAAAGGAGAAATGAGAGAGCGCATCGCTTTGGCAAAATCGCTTTGGGAGT 1380
Qy 383 GlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThrAsn 402
Db 1381 GGTTCAGTGTAACTCTCGCTGGAAGTGTAAACGTTACCGTACGATTAAAGACCTTAAGGAC 1440
Qy 403 SerProTrpGluHisCysLysLeuAspArgTyrProValLysIle 416
Db 1441 GGACCATGGTCCGATTGTATCGACCGTTACCGCTGTCTTTATT 1482
RESULT 11
US-09-058-947A-2
; Sequence 2, Application US/09058947A
; Patent No. 6274790
; GENERAL INFORMATION:
; APPLICANT: Kuest et al.
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
; TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell
; STREET: One World Trade Center, Suite
; STREET: 1600, 121 S.W. Salmon Street
; CITY: Portland
; STATE: OR
; COUNTRY: USA
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3 5-inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Word97 & ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058.947A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/043.831
; FILING DATE: April 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Earp, Ph.D.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 5493-50032/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 1807
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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US-09-058-947A-2

Alignment Scores:

Pedigree No.:	1.01e-137	Length:	1807
Score:	1259.50	Matches:	238
Percent Similarity:	73.67%	Conservative:	67
Best Local Similarity:	57.49%	Mismatches:	98
Query Match:	55.85%	Indels:	11
DB:	4	Gaps:	2

SEQ12-JOIN-SEQ4 (1-432) x US-09-058-947A-2 (1-1807)

QY	3	VallYrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerValSer	22
Db	323	ATCACCCTCGTGACTATCTTGTTACAGCAACCTGCTCAGCGTGTGCTCCCTCGCA	382
QY	23	LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr	42
Db	383	ACTTTCATGCAACACTCTCGTTGTATCTCTCAAG	415
QY	43	CysAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeuGly	62
Db	416	---GACAAAGCCTAAGAGCGTCGAGTCCAAATGAGATGCTTGAAGCTCTGGCTCGGT	472
QY	63	AspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAlaIa	82
Db	473	GAGGAGACTTGTCTCCCTCGCGGTATTCATTATATATCTCTCCACACCAACCATGGACGGC	532
QY	83	AlaArgGluGluThrGlnGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThr	102
Db	533	GCTAGAGCGAGGCTCAGATGTTTCTTCGAGGCGATGAGCAGTCTTTCAGAAACCC	592
QY	103	AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr	122
Db	593	GGTCTTAAACCTAAAGAGCTCGACATCCCTATTATCGTCAACTGCTCTCTTCTCTCCACCA	652
QY	123	ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe	142
Db	653	CCATCGCTCTCAGCTATGTCATCACAAAATATAGCTTAGGAGTAATATCAAGAGCTTC	712
QY	143	AsnLeuGlyClyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu	162
Db	713	ATCTTTCGGGGATGGCTGCGAGCGGGCCGTGATCTCAGTTGATCTAGCCCGCGAGCTTG	772
QY	163	LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsn	182
Db	773	CTCCAAGTCTATCCCAATTCAAATGCAATCATCTGTCAGCAGCAGATCATAAACGCTAAT	832
QY	183	IleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGly	202
Db	833	TACTATCAAGGCACGAGAGAGCCATGTTGTTACCCATTTGCTCTTCGATCGGGTGGC	892
QY	203	AlaAlaIleLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuVal	222
Db	893	GCACCCATACATGTTCTAAACCGCGGCTGTACCGGTGGGAGCCAAATATCAAGACTTTC	952
QY	223	HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGly	242
Db	953	CACCTCTCGGGACACCGTGGCGCTGAGCAGACAGTCTTCTACTGTGTTCTAGCAACAG	1012
QY	243	AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly	262
Db	1013	GAAGCAAAAGAGACAGCTGGCATCACTTGTCCAAAGATCTCATGGCCATCGCCGGT	1072
QY	263	ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLys	282
Db	1073	GAAGCCCTCAAGCAAAACATCACCACAATAGTCTTGTGTCCTACCGCGCTCAGAACAA	1132
QY	283	LeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyr	302
Db	1133	CTTCTCTTCTCAGTCCCTCATCGAGCATTAATCTTCAACCCGAAATGGAAACCA	1182
QY	303	TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisIaGlyGlyArgAla	322

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Query Match: 55.85% Indels: 11
DB: 4 Gaps: 2
SEQ12-JOIN-SEQ4 (1-432) x US-09-058-947A-1 (1-3722)

Qy 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHIsCysAsgValSerValSer 22
Db 2216 ATTCACCTCGTGTACTATCTGTGTACAGCCACCTGTCACGCTGTCGTCCTCCGTCGCA 2275
Qy 23 LysValMetAspIlePheTyrGlnIleAryLysAlaAspThrSerAryAsnGlyThr 42
Db 2276 ACTTTCATGGAACACTCTCGTTGATCTCTCAAG----- 2308
Qy 43 CysAspAspSerSerTrpLeuAspPheLeuAryLysIleGlnIuAryGSerGlyLeuGly 62
Db 2309 ---GACAAGCCTTAAGAGCGTCCAGTTCCTCAAAATGAGAATCTTGAACGTTCTGCGCTCGT 2365
Qy 63 AspGluThrHisGlyProGluGlyLeuLeuGlnValProProAryGlyThrPheAlaAla 82
Db 2366 GAGGAGACTGTCTCCCTCCGCGCTATTTCATATATATCTCCACACCAACCATGGACGCG 2425
Qy 83 AlaArgGluThrGlnGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThr 102
Db 2426 GCTAGAAGCGGCTCAGATGTTATCTTCGAGGCCATGAGCATCTTTTCAAGAAACCC 2485
Qy 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122
Db 2486 GGTCTTAAACCTTAAGAGCTCGACATCTTATGTCGCAACTGCTCTCTTTTCTCTCCACA 2545
Qy 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuAryGSerAsnValArySerPhe 142
Db 2546 CCATCGCTCTCAGCTATGCTCATCAACAAATATAAGCTTAGGAGTAAATATCAAGAGCTTC 2605
Qy 143 AsnLeuGlyMetGlyCysSerAryGlyValIleAlaLeuAspLeuAlaLysAspLeu 162
Db 2606 AATCTTCGGGATGGCTCGCGCGCGGCTGATCTCAGTTGATCTAGCCCGCGACTTG 2665
Qy 163 LeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsn 182
Db 2666 CTCCAAGTTCATCCCAATCAAAATGCAATCATCTGTCAGCGGAGATCATCAAGCCTAAT 2725
Qy 183 IleTyrAlaGlyAspAsnArgSerMetValSerAsnCysLeuPheAryGValGlyGly 202
Db 2726 TACTATCAAGGACGAGAGCGCATGTTGTTACCCATTTCTCTTCCGATGGGCGG 2785
Qy 203 AlaAlaIleLeuLeuSerAsnLysProGlyAspAryAryArySerLysTyrGluLeuVal 222
Db 2786 GCAGCCATACATGTCAAACCGCGGCTGACCGGTCGCGAGCAATACAAAGCTTTCC 2845
Qy 223 HisThrValArgThrHisThrGlyAlaAspGlyLysSerPheAryCysValGlnGly 242
Db 2846 CACTCTGTCGGACACCGCTGGCGCTGACGACAGTCTTCTACTGTGCTACGACAG 2905
Qy 243 AspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGly 262
Db 2906 GAAGCAAGAGGAGGACGCTGGCATCAACTGTCTCAAGATCTCATGGCCATCGCGCT 2965
Qy 263 ArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLys 282
Db 2966 GAAGCCCTCAGGCNAACATCACCAATAGTCTTTGGTCTTACCGGCTCGAACAA 3025
Qy 283 LeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleHisTyr 302
Db 3026 CTCTCTCTCCCTCAGCTCCCTAATCGGACGTAATAATCTTCAACCGGAATGGAACCA--- 3082
Qy 303 TyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyAryGAla 322
Db 3083 TACATACCGGATTCAGCTGGCTCGAACACTTTTGCATTCACGAGGAGGAGCGG 3142
Qy 323 ValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 342
Db 3143 GTGATCGAGCGAGCTCCAAAAGAACTTCAACATATCAGGAGAACACGTTGAGGCTCAAGA 3202
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Qy 343 SerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTrpTyrGluLeuAlaTyr 362
Db 3203 ATGACACTACATCGTTTGGTTAACACGCTCATCTTCATCGTTATGGTACGCTTAGCTAC 3262
Qy 363 IleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGlySer 382
Db 3263 ATCGAGTCTAAAGGGAGATGAGGAGAGCGATCGCTTTGGCAATCGCTTGGGAGT 3322
Qy 383 GlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThrAsn 402
Db 3323 GGTTCAGTGTAACTCTCCGCTGGAAATGTAAACGTTACGATTAAGACACCTAAGGAC 3382
Qy 403 SerProTrpGluHisCysLysIleAspArgTyrProValLysIle 416
Db 3383 GGACCATGGTCCGATGTATCCACCGTTACCGTGTCTTTATT 3424

RESULT 13
US-08-066-299-10
; Sequence 10, Application US/08066299
; Patent No. 5445947
; GENERAL INFORMATION:
; APPLICANT: James George Metz
; APPLICANT: Kathryn Dennis Lardizabal
; APPLICANT: Michael W. Lassner
; TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol
; TITLE OF INVENTION: O-Acyltransferases
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/066,299
; FILING DATE: 19930520
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/796,256
; FILING DATE: 20-NOVEMBER-1991
; APPLICATION NUMBER: 07/933,411
; FILING DATE: 21-AUGUST-1992
; APPLICATION NUMBER: PCT/US92/09863
; FILING DATE: 13-NOVEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-066-299-10

Alignment Scores:
Pred. No.: 1,42e-137 Length: 1733
Score: 1258.00 Matches: 244
Percent Similarity: 75.00% Conservative: 68
Best Local Similarity: 58.65% Mismatches: 92
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Query Match: 55.79% Indels: 12
DB: 1 Gaps: 4
SEQ12-JOIN-SEQ4 (1-432) x US-08-066-299-10 (1-1733)
Qy 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerValSer 22
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 GTCTACTTGGTGGACTTGGATGCTATAAGCTCAACCGACCTGATGATCATCCACGAG 428
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 23 LysValMetAspPheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 429 ATGTCATG-----GACCGACCTCCCGGGCGGGTCG 461
Qy 43 CysAspAspSerSerTyrLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeuGly 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 462 TTTTCTAAGGAGAT---ATTGAGTTTCAGAGGAAGATCTTGAGAGGCGCGGTATGGGT 518
Qy 63 AspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAlaAla 82
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 519 CGGGAACCTATGTCCTCCGAATCCGTCACATAAGGTGCCCGCGAGCCGATACGACGA 578
Qy 83 AlaArgGluGluThrGlnGlnValIleGlyAlaLeuGluAsnLeuPheLysAsnThr 102
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 579 GCCAGGCGCGAGCGGAGGAGGTATGATACGGGGCGATCGACGAGGTGTGGAGAAGACG 638
Qy 103 AsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnProThr 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 639 GGGGTGAAGCGGAGCAGATAGATAGTACTGGTGTGACTGCTGCTGTTTAAACCCACG 698
Qy 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 699 CGGTGCTGTCATCCATGATAGTAAACCATTAACAGCTNAGGGGTAAATATAGTCTAT 758
Qy 143 AsnLeuGlyMetGlyCysSerIleGlyValIleAlaLeuAlaLeuAlaLysAspLeu 162
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 759 AATCTGTGGTGATGGGTGGCATGCGAGTGGTGTAGTGTAGTGGAGCGGAAACATGACCTC 818
Qy 163 LeuHisValHis---LysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 819 CTACAGGTTTACCTGTAACCAACATATGTTAGTGTAGTGGAGCGGAAACATGACCTT 878
Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 879 AATGTGTACTGGGCAATACCGCTCCATGCTTATACCAACTGCTATTCGCATGGGT 938
Qy 202 GlyAlaLarLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 939 GCGCTGCCATCATCTCTCAAAACCGTGGCGTGTGCTGATCGCGGATCCAAGTACCACTC 998
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 999 CTTCATACGTACGCCCAACAGGCGGTGACGACGAAGTCCCTATAGATGCGCTTACAA 1058
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLysLysAspIleThrAspValAla 261
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1059 CAAGAAGATGAATAACAAGGTAGGTGTGCTTATCCAAGGATCTGATGGCAGTTGCC 1118
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1119 GGTGAAGCCCTTAAAGGCCAATACATGACGACCTTGTGCTGCTGCTGCTGCTGCTGCTG 1178
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1179 CAACTCTCTTCTTGGCACCTTAGTGGCAGCTAAGGTCTTCAAGATGACGAACGTGAAG 1238
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1239 CCATACATCCAGATTTCAAAGTTGGCGGAGCAACGACTTCTGATPCCATCGAGGAGCAAA 1298
Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1299 GCAGTGTGGTGAAGCTCGAAGAAGAACTGGAGTTGACGCCATGGCACCTTGAACCTCG 1358

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,047
FILING DATE: 23-JUN-94
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/160,602
FILING DATE: 30-NOV-93
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/796,256
FILING DATE: 20-NOV-91
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/933,411
FILING DATE: 21-AUG-92
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/066,299
FILING DATE: 20-MAY-93
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09863
FILING DATE: 13-NOV-92
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 101-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2 :
SEQUENCE CHARACTERISTICS:
LENGTH: 1733 base pairs
TYPE: nucleic acid
```

STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-265-047-2

Alignment Scores:

Pred. No.: 1,42e-137 Length: 1733
 Score: 1258.00 Matches: 244
 Percent Similarity: 75.00% Conservative: 68
 Best Local Similarity: 58.65% Mismatches: 92
 Query Match: 55.79% Indels: 12
 Ds: 1 Gaps: 4

SEQ12-JOIN-SBQ4 (1-432) x US-08-265-047-2 (1-1733)

Qy 3 ValTyrLeuValAspTyrSerCysTyrLeuProProHIsCysArgValSerValSer 22
 Db 369 GTCTACTGTTGGTGGATGCTATAGCCCTCAACCGACCTGATGACATCCACGAG 428
 Qy 23 LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr 42
 Db 429 ATCTTCATG-----GACCGAGACTCCCGGGCGGGTGG 461
 Qy 43 CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeuGly 62
 Db 462 TTTTCTAAGGAGAAAT---ATTGAGTTTCACAGAGAGATCTTGGAGAGGGCGGTATGGGT 518
 Qy 63 AspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAlaAla 82
 Db 519 CGGGAACCATGATGCCCGAATCCGCTACTAAGGTGCCCGCGAGCGAGCATAGCAGCA 578
 Qy 83 AlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThr 102
 Db 579 GCCAGGCGCGAGGAGGAGGTGTACGGGCGATCGACGAGGTGTGGAGAGACG 638
 Qy 103 AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr 122
 Db 639 GGGGTGAACGACGACAGTAGAATACTGGTGGTGACTGCTGCTGTTTAAACCCAAACG 698
 Qy 123 ProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPhe 142
 Db 699 CGCTCGCTGTCATCATGATAGTAAACCATTAACAGCTNAGGGGTATATATACCTAT 758
 Qy 143 AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu 162
 Db 759 ATCTTGGTGGATGGGTGGAGTGGCTGCTATTCATGATGCTGCAAGGACCTC 818
 Qy 163 LeuHisValHis---LysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
 Db 819 CTACAGGTTTACCGTAAACACACATATGTTAGTAGTACGACGGAACATGACCTT 878
 Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 Db 879 AATTGGTACTGGGCAATGACCTCCATGCTTATCACAACCTGCCCTATTTCCATGGGT 938
 Qy 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
 Db 939 GGGCTGCCATCTCTCAAAACCGCTGGCTGATGCTGCCGATCCCAAGTACCACTC 998
 Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
 Db 999 CTTCATACAGTACGACCCCAAGGCGCTGACGACAACTGCTATAGATCGGCTTACAA 1058
 Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
 Db 1059 CAAGAAGATGAAATAACAAGTAGGTGTTGCTTATCCAAAGGATCTGATGGCGAGTTGC 1118
 Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
 Db 1119 GGTGAGCCCTTAAGGCCACATACAGACCTTGTGCTCCCTCGGCTCCCACTGTCAGAA 1178
 Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
 Db 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301

Db 1179 CAACCTCTCTCTCTTCCACCTTAGTGGCAGCTAGAGTCTTCAAGATGACGAACGTGAAG 1238
 Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
 Db 1239 CCATACATCCAGATTTCAAGTTGGCAGCAACGACTTCTGTCATCCTCAGAGGCAAA 1298
 Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
 Db 1299 GCAGTGTGGATGAGCTCGAGAGAACTTGGAGTTGACGCCATGGCACCTTGAACCCCTC 1358
 Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTrpTyrGluLeuAla 361
 Db 1359 AGGATGACACTGTATAGTTTGGAAACACATCGAGTAGCTCATATTGTTACGAGTTGCA 1418
 Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
 Db 1419 TACGCTGAACGAAGAGGAGGATCGTGGAGGCTTGTGGAGGAGTGTCAATCCGCTAGA 1478
 Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLys---AlaSer 400
 Db 1479 TCAGGTTTCAAGTGAACAGTGTGTGTGGAGGCTTGTGGAGGAGTGTCAATCCGCTAGA 1538
 Qy 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIle 416
 Db 1539 GAGAAGATCCTTGGATGATGAATTTGAGAAGTTCCTCTCTCATGTG 1586

RESULT 15

US-08-926-522-21
 ; Sequence 21, Application US/08926522
 ; Patent No. 6426447
 ; GENERAL INFORMATION:
 ; APPLICANT: Vic C. Knauf
 ; APPLICANT: Gregory A. Thompson
 ; TITLE OF INVENTION: PLANT SEED OILS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Calgene, Inc.
 ; STREET: 1920 Fifth Street
 ; CITY: Davis
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 95616
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.1
 ; SOFTWARE: Microsoft Word 5.1(a)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08926,522
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/458,173
 ; FILING DATE: 2-June-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elizabeth Lassen
 ; REGISTRATION NUMBER: 31,845
 ; NAME: Donna E. Scherer
 ; REGISTRATION NUMBER: 34,719
 ; NAME: Carl J. Schwedler
 ; REGISTRATION NUMBER: 36,924
 ; REFERENCE/DOCKET NUMBER: CGNE DES
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (916) 753-6313
 ; TELEFAX: (916) 753-1510
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1733 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; US-08-926-522-21

Alignment Scores:

Fragment Location:		
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Score:	1258.00	244
Percent Similarity:	75.00%	Conservative: 68
Best Local Similarity:	58.5%	Mismatches: 92
Query Match:	55.79%	Indels: 12
DB:	4	Gaps: 4

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Db	369	GTCTACTTGGTGAATCTTGGATGCTATAAGCTTCAACCAACCTGATGACATCCACGAG	428
Qy	23	LysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGlyThr	42
Db	429	ATGTTTCATG-----GACCGGACCTCCCGGGCCGGGTGCG	461
Qy	43	CysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnLysSerGlyLeuGly	62
Db	462	TTTCTTAAGAGAAAT--ATTGAGTTTCAGAGGAAGATCTTGAGAGGCCCGGTATGGGT	518
Qy	63	AspGluThrHisGlyProGlnGlyLeuLeuGlnValProArgLysThrPheAlaAla	82
Db	519	CGGGAAACCTATGTCCTCCGAATCTACTAAGGTGCCCGCGGCGGAGCATAGCACA	578
Qy	83	AlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThr	102
Db	579	GCCAGGGCCGAGCGGAGGAGTGATGTACGGGGCGATCGACGAGGTGTGGAGAAGACG	638
Qy	103	AsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThr	122
Db	639	GGGGTCAAGCCGAGCAGATAGGAATACTGTGTGTCGANTCGCAGCTGTTTAAACCCAACG	698
Qy	123	ProSerLeuSerAlaMetValAlaAsnThrPheLysLeuArgSerAsnValArgSerPhe	142
Db	699	CGCTCGCTGTCTCATCATGATAGTAGTAAACATATACAACTNAGGGGTAAATATCTAGTGAT	758
Qy	143	AsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeu	162
Db	759	AATCTTGTGTGCATGGGTTCAGTGTGGCTCATTTCCCATTCATCTTGCCAAAGSACCTC	818
Qy	163	LeuHisValHis---LysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr	181
Db	819	CTACAGGTTTACCCTAAACACATATGTGTAGTAGTGAGCAGGAAACATGACCCCT	878
Qy	182	AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly	201
Db	879	AATGTGTACTGGGCAATGACCGCTCCATGCTTTATACCAACTGCCTATTTCCGATGGGT	938
Qy	202	GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrCluLeu	221
Db	939	GGCGTGCATCATCTCTCAACACGCTGGGTGATCGTCCCGATCCCAAGTACCACATC	998
Qy	222	ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln	241
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Qy	242	GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla	261
Db	1059	CAGAGAGATGAATAACAGAGTAGTGTTGCCTTATCCAAAGATCTGATGGCAGCTGCCC	1118
Qy	262	GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu	281
Db	1119	GGTGAAGCCCTTAAGAGCCCAACATCACACCTTGTGTCCTGCTGCCATGCCATGTCAGAA	1178
Qy	282	LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis	301
Db	1179	CAACTCTCTTCTTGGCCACCTTAGTGGCAGCTAAGGTCTTCAAGATGAGCAACGTGAAG	1238
Qy	302	TyrTyrValProAspPheLysLeuAlaThrLeuAspHisPheCysIleHisAlaGlyArg	321

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2003, 18:10:06 ; Search time 49.5 Seconds

(without alignments)

3774.584 Million cell updates/sec

Title: SEQ12-JOIN-SEQ4

Perfect score: 2255

Sequence: 1 NPYLVDSYCLPPPHCRVS.....PVKIDSDSKSETRVQNGRS 432

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications.NA -QEXT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62
-TRANS=human40.cdi -LIST=45 -LOCALALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications.NA.*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2243	99.5	1521	10	US-09-877-476-11
3	2239	99.3	1521	10	US-09-877-476-13

4	2238	99.2	1521	10	US-09-877-476-21
5	2235	99.1	1521	10	US-09-877-476-15
6	2232	99.0	1521	10	US-09-877-476-7
7	2208.5	97.9	1518	10	US-09-877-476-9
8	2208.5	97.9	1524	10	US-09-877-476-3
9	2201.5	97.6	1518	10	US-09-877-476-17
10	2201.5	97.6	1524	10	US-09-877-476-33
11	2177	96.5	1521	10	US-09-877-476-25
12	2176	96.5	1521	10	US-09-877-476-39
13	2156.5	95.6	1521	10	US-09-877-476-31
14	2156	95.6	1521	10	US-09-877-476-23
15	2155	95.6	1521	10	US-09-877-476-37
16	2153.5	95.5	1736	10	US-09-877-476-5
17	2149.5	95.3	1521	10	US-09-877-476-41
18	2056	91.2	1521	10	US-09-877-476-29
19	2039.5	90.4	1521	10	US-09-877-476-27
20	2013	89.3	1709	10	US-09-877-476-35
21	2010	89.1	1709	10	US-09-877-476-1
22	1519.5	67.4	1611	10	US-09-883-797-9
23	1503.5	66.7	1548	10	US-09-883-797-3
24	1487.5	66.0	1479	10	US-09-883-797-13
25	1473.5	65.3	1512	10	US-09-883-797-5
26	1273	56.5	1530	9	US-09-938-842A-1205
27	1259.5	55.9	1491	10	US-09-892-325-3
28	1259.5	55.9	1494	9	US-09-938-842A-569
29	1259.5	55.9	1502	10	US-09-883-797-11
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32	1241.5	55.1	1560	10	US-09-883-797-1
33	1241.5	55.1	1563	9	US-09-938-842A-1552
34	1235	54.8	1587	9	US-09-938-842A-1598
35	1120	49.7	1653	9	US-09-938-842A-2597
36	1119	49.6	1650	10	US-09-883-797-7
37	1059	47.0	2782	10	US-09-905-657-1
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39	502	22.3	468	10	US-09-770-444-253
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41	420	18.6	409	10	US-09-878-574-4051
42	371	16.5	387	10	US-09-878-574-1065
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45	183.5	8.1	3114	9	US-10-037-598-35

ALIGNMENTS

RESULT 1
US-09-877-476-11
; Sequence 11, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ IDS NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3) having mutations at positions 271, 272 and
; NAME/KEY: CDS
; LOCATION: (1)...(1518)

```

Db      1123  CATTACTAGTCCTCCGGATTTCAAACTTCCTATTGACCAATTTTGTATACATGCCGGAGGC 118
QY      321  ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db      1183  AGAGCCGCTGATTGATGCTGTAGAGAAGAACCTAGCCCTAGCACCGCATCGATGTAGAGSCA 1242
QY      341  SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrGluLeu 360
Db      1243  TCAAGATCAACCTGTACATAGATTGGAAACAACCTCATCTAGCTCANATGCTATGATGATG 1302
QY      361  AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
Db      1303  GCATACATAGAAGCAAAAGAGGATGAAGAAGTAAAGTTAAAGTTGCGAGATTCGTTTA 1362
QY      381  GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
Db      1363  GGGTCAGGCTTTAGTGTACAGTGCAGTGGGTGGCTCTAAACATGTCAAAAGCTTCG 1422
QY      401  ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db      1423  ACAAAATAGTCCCTGGGAACACTGCATCGACAGATPACCCGGTCAAAATTTGATTCTGATTCA 1482
QY      421  GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db      1483  GGTAAAGTCAGAGACTCGTGTCCCAACGGTCGGTCC 1518

RESULT 2
US-09-877-476-19
; Sequence 19, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
;   APPLICANT: Jaworski, Jan G.
;   TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
;   TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
;   FILE REFERENCE: 07148-108001
;   CURRENT APPLICATION NUMBER: US/09/877,476
;   CURRENT FILING DATE: 2001-06-08
;   PRIOR APPLICATION NUMBER: US 60/210,326
;   PRIOR FILING DATE: 2000-06-08
;   NUMBER OF SEQ ID NOS: 56
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 19
;   LENGTH: 1521
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
;   OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID
;   OTHER INFORMATION: NO:3) having mutations at positions 271, 272, 275
;   OTHER INFORMATION: and 920; designated At14L91C K92R G307D;
;   OTHER INFORMATION: hypothetical
;   NAME/KEY: CDS
;   LOCATION: (1)...(1518)
US-09-877-476-19

Alignment Scores:
Pred. No.:      2,42e-263      Length:      1521
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Percent Similarity: 99.77%      Conservative: 1
Best Local Similarity: 99.54%      Mismatches: 1
Query Match:      99.47%      Indels: 0
DB:              10      Gaps: 0

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Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
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Db 463 CGCGCGCGCGTGAAGACGAGCAAGTATCATCTGGTGGCTAGAAATCATTTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAAGCTTAAACCTTAAGATATAGTATCTTGGTGAATCAAGCATGTTTAAT 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCATCGCTCCGCGATGCTGTTAACACTTCAAGCTCCGAACCAACGTAAGA 642
Qy 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACTTGGTGGCATGGGTGTGAGCGCGGTATAGCCATGATGATAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTGTCATGTCATAAAAATACGATATGCTCTTGTGGTGAGCAGACATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
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Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGCGCGCTATTTGCTCTCAACAACGCTGGAGATCGTAGACGGTCCAAAGTACGAG 882
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTCACACGGTTCGAACCATACCGGAGCTGAGCACAAGTCTTTTCGTTGGTGCAA 942
Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGACAGCAGTGAAGCGCAAAATCGGAGTGAAGTTCCTCCAGCAGCATTAACCGATGT 1002
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGGTCGAACGGTTAAGAAAAACATAGCAACGTTGGGTCGTTGATTCCTCGTTAAGC 1062
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Db 1243 TCAAGATCAACGTTACATAGATTTGGAACACTTCATCTAGCTCAATATGATGATGAGTTG 1302
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Qy 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
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; Sequence 13 Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 342 bp from A. thaliana FAEL (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3), having a mutation at position 275;
; OTHER INFORMATION: designated At114 K92R
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-13
Alignment Scores:
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Score: 2239.00 Matches: 430
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Best Local Similarity: 99.54% Mismatches: 2
Query Match: 99.29% Indels: 0
Gaps: 0
DB:
SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-13 (1-1521)
Qy 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSer 20
Db 223 AATCCGGTTTATCTCTTGACTACTCGTGTGTACCTTCCGCCACCGCATCTCAGAGTTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db 283 GTCTCTAAAGTCATGGATATTTCTACCAATAAGAAAGCTGATCTTCTTACGGAAC 342
Qy 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
Db 343 GGCACGTGTGATGATTCGTCGGCTTGACTTCTTGGGAAGATTCAAGAACGTTTCAGGT 402
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGGCGATGAACCTACGCGCGCGAGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTT 462
Qy 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 CGCGCGCGCGTGAAGACGAGCAAGTATCATCTGGTGGCTAGAAATCATTTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAAGCTTAAACCTTAAGATATAGTATCTTGGTGAATCAAGCATGTTTAAT 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140

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Db 583 CCAACTCCATCGCTCCGGCGTGGTTCGTTAACTTTCAAGCTCCGAAGCAACGTAAGA 642
Qy 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACTTGGTGGCATGGGTGTAGTGGCGGCTTATAGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValSerThrGluAsnIleThr 180
Db 703 GACTTTGTCATGTCATATAAATACGTATGCTTGTGGTGAGCAGAGAACATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGGTGATATAGTCCATGATGGTTTCAAAATGCTTGTCCGTTG 822
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGGCGCTATTTTCTCCCAACAAGCTGAGATCGTAGCGTCCAAAGTACGAG 882
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTACACCGGTTCCGACGCATACCGGAGCTGACGGCAAGTCTTTTCGTTGCGTCAA 942
Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLysLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGAGACGATGAGAACGCGCAAAATCGGAGTGGTTCCTCCAAAGGACATAACCGATGTT 1002
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGGTCCGAACGGTTAAGAAAACATAGCAACGTTGGTCCGCTGATCTTCCGTTAAGC 1062
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
Db 1063 GAGAACTCTCTTTTTCGTTACCTTCATGGCAAGAACTTTTCAAGATATAAATCAA 1122
Qy 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
Db 1123 CATTAAGTACGTCGCGGATTTCAAACTTGCTATTGACCATTTTGTATACATGCGGAGGC 1182
Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGACCGGTGATGATGCTGTAGAGAAGCACTAGCCCTAGCACCATCGATGATGAGGCA 1242
Qy 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTyrTyrGluLeu 360
Db 1243 TCAAGATCAACGTTACATAGATTTTGGAAACACTTCATCTAGCTCAATATGTTATGATG 1302
Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
Db 1303 GCATACATAGAACAAAGGAAGGATGAGAAAGGTAAATAAGTTTGGCAGATTGCTTTA 1362
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer 400
Db 1363 GGGTCAGCGCTTAAAGTGAACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAAGCTTCG 1422
Qy 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAATAGTCTTGGGACACTGTCATCGACAGATACCGGTCCAAATTTGATTCGATTCA 1482
Qy 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAAGTCAGAGACTCGTGTCCCAAAACGGTGGTCC 1518
```

RESULT 4

```
US-09-877-476-21
; Sequence 21, Application US/09877476
; Patent No. US20020499941
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
```

```
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO.3) having mutations at positions 275 and 920;
; OTHER INFORMATION: designated At114 K92R G307D; hypothetical
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
; US-09-877-476-21
```

```
Alignment Scores:
Pred. No.: 9,83e-263 Length: 1521
Score: 2238.00 Matches: 430
Percent Similarity: 99.54% Conservative: 0
Best Local Similarity: 99.54% Mismatches: 2
Query Match: 99.25% Indels: 0
DB: 10 Gaps: 0
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SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-21 (1-1521)

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Qy 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSer 20
Db 223 AATCGGGTTTACTCTCGTTGACTACTCGTTTACCTTCGCCACCGCATCTCAGAGTTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db 283 GTCCTAAAGTCATGGATAFTTTCTACCAATAGAAAAGCTGATACTTCTTCACGGAAC 342
Qy 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
Db 343 GGCACGCTGTGATGATTCGTCGTGGCTTGACTTCTTTGAGGAAGATTCAAGAACGTTCAAGT 402
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGCGGATGAACACTCACGGGCGGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTT 462
Qy 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCGGCGGCGCTGAAGAGACGAGCAAGTTATCATTTGGTGGCTAGAAAAATCTATTTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 ACACCAACGTTTAACTTAAAGATATAGGTATAGTATAGTATAGTATAGTATAGTATAGT 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCATCGCTCCCGCATGGTGGTTCGTTTAACTTTTCAAGCTCCGGAACCAACGTAAGA 642
Qy 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACTTGGTGGCATGGGTTCGTTAGTGGCGGCTTATAGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTTCATGTCCATATAAATACGTATGCTTGTGGTGAGCAGAGAACATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGGTGATATAGTCCATGATGGTTTCAAAATGCTTGTTCGTTGTT 822
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGGCGCTATTTTGTCTCTCCAAACAAGCTGGAGATCGTAGACGCTCAAGTACGAG 882
```



```
QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTCACAGGTTCCGACGATACCGGAGCTGACGACAAGTCTTTTCGTCGTCGCAA 942
QY 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGAGACGATGAGAACGGCAAAATCGGAGTGAGTTGTTCACAGGACATAACCGATGTT 1002
QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGGTCCGACGGTTAAGAAAAACATAGCAAGTTGGGTCGTTGATCTTCGTTAAGC 1062
QY 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
Db 1063 GAGAACTCTCTTTTTCGTTACCTTCATGGCGCAAGAACTTTTCAAGAGATAAAATCAAA 1122
QY 301 HisTyrTyrValProAspPheLysLeuAlaIleAspPheLysPheCysIleHisAlaGlyGly 320
Db 1123 CATTACTAGCTCCGGATTTCAAACTTGCTATTGACCATTTTGTATACATGCCGGAGGC 1182
QY 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGACCGGTGATGATGCTAGAGAAAGAACCTAGCCCTAGCACGATCGATGATGAGGCA 1242
QY 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTTPTrpGluLeu 360
Db 1243 TCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATGCGTATGAGTTG 1302
QY 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
Db 1303 GCATACATAGAAAGCAAGGAGGATGAAGAAAGGTAATAAAGTTTGGCAGATGCTTTA 1362
QY 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
Db 1363 GGGTCAGGCTTAAAGTCTAACAGTCAGCTTTGGGTGGCTCTAAACAATGTCAAAGCTTCG 1422
QY 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerSer 420
Db 1423 ACAATATGCTCTGGGAACACTGCATCGACAGATACCCGGTCAAAATGATTCGTGATCA 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAGTCAGAGACTCGTGTCCAAAACGGTCGGTCC 1518
```

RESULT 5

```
US-09-877-476-15
; Sequence 15, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 342 bp from A. thaliana FAEL (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3), having a mutation at position 920;
; OTHER INFORMATION: designated At14 G307D; hypothetical
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-15
```

```
Alignment Scores:
Pred. No.: 2,28e-262 Length: 1521
Score: 2235.00 Matches: 429
Percent Similarity: 99.54% Conservativity: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.11% Indels: 0
DB: 10 Gaps: 0
```

SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-15 (1-1521)

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QY 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSer 20
Db 223 AATCCGGTTTATCTGCTGACTACTCGTGTGTACCTTCGCGCACCGCATCTCAAGTAGT 282
QY 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db 283 GTCTCTAAAGTCATGATATTTCTACCAATAAGAAAGCTGATACTTCTTCACGGAAC 342
QY 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnIuArgSerGly 60
Db 343 GGCACGTGTGATGATCGTGTGGTTCGACTTCCTTGAGGAAGATTCAAGACGTTCAAGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGGCGATGAACACTCACGGGCGCGAGGGGCTGCTTCGGTCCCTCCCGGAAGACTTTT 462
QY 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 CGCGCGCGCGTGAAGAGACGGAGCAAGTTATCATTTGGTGGCTAGAAAAATCATTTCAAG 522
QY 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAACGTTAAACCTTAAGATATAGGTATACTTGTGGTGAACCTCAAGCATGTTTAA 582
QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCATCGCTCTCCCGCATGTGCTTAACTTCAAGCTCCGAAGCAAGCAAGTAAGA 642
QY 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACTTGTGGTCATGGTGTGTAGTGCCGCGTTATAGCCATTGATCTAGCAAG 702
QY 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTTCATGTCATCAATAAATACGTATGCTCTTGTGGTGAGCACAGACAATCACT 762
QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTAGCTGTGATAATAGGTCCCATGATGGTTTCAAAATGCTTGTTCGTTGTT 822
QY 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGCGCGTATTTGCTCTCCAAAGCCTGGAGATCGTAGACGGTCCCAAGTACGAG 882
QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTCCACAGGTTTCGACGACATACCGGAGCTGACGACAACTCTTTTCGTTGGTGC 942
QY 241 GluGlyAspAspLysAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGAGACGATGAGAACGGCAAAATCGGAGTGGATGTTGTTCACAGGACATAACCG 1002
QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGGTCCGACGGTTAAGAAAAACATAGCAAGTTGGGTCGTTGATCTTCGTTAAGC 1062
QY 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
Db 1063 GAGAACTCTCTTTTTCGTTACCTTCATGGCGCAAGAACTTTTCAAGAGATAAAATCAAA 1122
QY 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
Db 1123 CATTACTAGCTCCGGATTTCAAACTTGCTATTGACCATTTTGTATACATGCCGGAGGC 1182
```


QY 421 GlySerGluThrArgValGlnAsnGlyArgSer 432
 |||||
 Db 1483 GGTRAGTCAGACTCGGTGTCCTCAACAGGGTCGCTCC 1518

RESULT 7

US-09-877-476-9
 ; Sequence 9, Application US/09877476
 ; Patent No. US20020049994A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Blacklock, Brenda J.
 ; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
 ; FILE OF INVENTION: SYNTHASE POLYPEPTIDES
 ; FILE REFERENCE: 07148-108001
 ; CURRENT APPLICATION NUMBER: US/09/877,476
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,326
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 1518
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: 5' 222 bp from A. thaliana FAEL (SEQ ID NO:1) and
 ; OTHER INFORMATION: 3' 1296 bp from B. napus elongase KCS (SEQ ID
 ; OTHER INFORMATION: NO:3); designated At74
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1515)
 ; US-09-877-476-9

Alignment Scores:
 Pred. No.: 3,84e-259 Length: 1518
 Score: 2208.50 Matches: 424
 Percent Similarity: 99.07% Conservative: 3
 Best Local Similarity: 98.38% Mismatches: 1
 Query Match: 97.94% Indels: 1
 DB: 10 Gaps: 1

SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-9 (1-1518)

QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerVal 21
 |||||
 Db 226 CCGGTTTACCTCGTGTAGTACTCATCTACCTCCACCAAGCATTTAGTACATC 285
 QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41
 |||||
 Db 286 TCCAGGTCATGGGATATCTTTTATCAAGTAGAAGAAAGCTGAT---CCTTCTCGGAACGGC 342
 QY 42 ThrCysAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
 |||||
 Db 343 ACGTGCATGACTCGTGTGCTGCTTCTTGTAGAGAGATTCAGAAACGTTTCAGTCTA 402
 QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
 |||||
 Db 403 GCGGATGAATCACTACGGGCGGAGGGGCTGCTTCAAGTACAGGTCCTCCCGGAGACTTTTTCG 462
 QY 82 AlaAlaArgGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
 |||||
 Db 463 CCGGCGCTGAAGAGACGAGCAAGTATCATCTGTCGCTAGAAAATCTATTTCAGAAC 522
 QY 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
 |||||
 Db 523 ACCAAGTTAACCCATAAGATATAGTATACCTTGTGGTGAAGTCAAGCATGTTTAATCCA 582
 QY 122 ThrProSerLeuSerAlaMetValAsnThrPheLysLeuArgSerAsnValArgSer 141
 |||||
 Db 583 ACTCCATCGCTCTCCGGATGGTCTTACACTTTCAGCTCCGAGCAACGTTAGAGAC 642
 QY 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
 |||||

Db 643 TTTAACCTTGGTGGCATGGGTTGTAGTCCGGCGTTATAGCCATTGATCTACGAAGAC 702
 QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValSerThrGluAsnIleThrTyr 181
 |||||
 Db 703 TTGTTGCATGTCCATAAAAAATACGTATGCTCTTGTGGTGACACAGAACATCACTAT 762
 QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 |||||
 Db 763 AACATTTACGCTGGTGATATAGGTCCATGATGTTTCAAAATGCTTGTGTCGTTGGT 822
 QY 202 GlyAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
 |||||
 Db 823 GGGGCGCTATTTTGTCTCCAAACAGCTGGAGATCGTAGCGTCCCAAGTACGAGCTA 882
 QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
 |||||
 Db 893 GTTCACACGGTTCGAACGATACCGGAGCTGACGCAAGTCTTTTCGTTGCGTGCAACA 942
 QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
 |||||
 Db 943 GGAGACGATGAGAACGCAAAATCGAGTGTGTTGTCCAAGGACATAACCGATGTCCT 1002
 QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
 |||||
 Db 1003 GGTGCAACGGTTAAGAAAAACATACCAACGTTGGTCCGTGATCTTCCGTTAAGCGAG 1062
 QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
 |||||
 Db 1063 AAACCTCTTTTTCGTTACCTTCATGGCAAGAAACTTTTCAAGATAAATAACAT 1122
 QY 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
 |||||
 Db 1123 TACTACGTCGGGATTCAAACTGCTATGACCACTTTTGTATACATCCGAGGCGAGA 1182
 QY 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
 |||||
 Db 1183 GCCGTGATTGATGCTGTAGAGAAGAACCTAGCCCTAGCAGCATCATGTAGAGCATCA 1242
 QY 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleThrPyrGluLeuAla 361
 |||||
 Db 1243 AGATCAACGTTACATAGATTTGGAACACTTCATCTAGCTCATATGTTAGTTGGCA 1302
 QY 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
 |||||
 Db 1303 TACATAGAACAAGAAAGAGGATGAAGAAAGGTATATAAGTTTGGCAGATTGCTTTAGGG 1362
 QY 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr 401
 |||||
 Db 1363 TCAGGCTTTAAGTGTAAACAGTCAGTCTTTGGTGGCTCTAAACAATGTCAAAGCTTCGACA 1422
 QY 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
 |||||
 Db 1423 ATATGTCCTTGGGAACACATGACATCGACAGATACCGGTCAAAATGATCTGATTCAGGT 1482
 QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
 |||||
 Db 1483 AAGTCAGAGACTCGTGTCCAAAACGGTCGGTCC 1515

RESULT 8

US-09-877-476-3
 ; Sequence 3, Application US/09877476
 ; Patent No. US20020049994A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Blacklock, Brenda J.
 ; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
 ; FILE OF INVENTION: SYNTHASE POLYPEPTIDES
 ; FILE REFERENCE: 07148-108001
 ; CURRENT APPLICATION NUMBER: US/09/877,476
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,326
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 1524

; TYPE: DNA

; ORGANISM: Brassica napus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1521)

US-09-877-476-3

Alignment Scores:

Pred. No.:	3,87e-259	Length:	1524
Score:	2208.50	Matches:	424
Percent Similarity:	99.07%	Conservative:	3
Best Local Similarity:	98.38%	Mismatches:	1
Query Match:	97.94%	Indels:	1
DB:	10	Gaps:	

SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-3 (1-1524)

Qy	2	ProValTyrLeuValAspTyrSerCysTyrLeuProTyrHisCysAtgValSerVal	21
Db	229	CCGGTTTACCTGGTGGTACTCATGCTACCTCCACCAACCATTTGTAGATCAAGTATC	288
Qy	22	SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly	41
Db	289	TCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAGCTGAT--CCCTCTCGGAACGGC	345
Qy	42	ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu	61
Db	346	ACGTGGGATGACTCGTGGTGGCTTGCTTTCAGGAGATTCAGAAACGTTTCAGGCTA	405
Qy	62	GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla	81
Db	406	GGCGATGAACACTCAGCGGCGGAGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTGGC	465
Qy	82	AlaAlaArgGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn	101
Db	466	CGCGCGGTGAAGACGAGCAAGTTATCATTTGGTGGCTAGAAATCTATTCAACAAC	525
Qy	102	ThrAsnValAsnProLysAspIleGlyLeuValAsnSerSerMetPheAsnPro	121
Db	526	ACCAAGTTAAACCTTAAGATATAGGTATACCTTGGTGAACCAAGCATGTTTAAATCCA	585
Qy	122	ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer	141
Db	586	ACTCCATCGCTCTCCGCGATGGTGTAAACACTTTTCAAGCTCCGAAGCAACGTAAGAAGC	645
Qy	142	PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp	161
Db	646	TTTAAACCTGGTGGCATGGGTGTAGTCCCGGGCTTATAGCCATTGATCTAGCAAGGAC	705
Qy	162	LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr	181
Db	706	TTGTTGCATGTCATAAAAATACGTATGCTCTTGTGGTGAGCACAGAGAATCATCACTAT	765
Qy	182	AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly	201
Db	766	AACATTTACCGTGGGTATAGGTGCTCATGATGATGTTTCAAAATGCTTGTCCGTTGGT	825
Qy	202	GlyAlaAlaIleLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu	221
Db	826	GGGCGCCGCTATTTGCTCTCCAAACAGCTGGAGATCGTAGAGCTCCCAAGTAGGAGCTA	885
Qy	222	ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln	241
Db	886	GTTCCACAGGTTCCAGACGATACCGAGCTGACGGCAAGTCTTTTCGTGGTGCACAA	945
Qy	242	GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla	261
Db	946	GGAGACGATGAGAACCGCAAAATCGGAGTGGTGTGCTTCCAAAGGACATAACCGCATGTTGCT	1005
Qy	262	GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu	281

Db	1006	GGTCGAACGGTTAAGAAAAACATAGCAACGGTTGGTCCGTTGATTCTCCGTTAAGCGAG	1065
Qy	282	LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLysHis	301
Db	1066	AAACTTCTTTTTCGTTACCTTCATGGCAAGAAACTTTTCAAGATAAATCAACAT	1125
Qy	302	TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArg	321
Db	1126	TACTACGTCGCGGATTTCAAACTTGTGACCATTTTGTATACATCCGAGGCGAGA	1185
Qy	322	AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer	341
Db	1186	GCCTGATGATGCTAGAGAAAGAACTAGCCCTAGCAGCATGATAGAGGCATCA	1245
Qy	342	ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleThrPyrGluLeuAla	361
Db	1246	AGATCAACGTTTACATAGATTTGGAACACTTCATCTAGCTCAATATGGTATGAGTTGCA	1305
Qy	362	TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly	381
Db	1306	TACATAGAACCAAGAGGATGAGAAAGGTAAATAAGTTGGCAGATTGCTTTAGGG	1365
Qy	382	SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr	401
Db	1366	TCAGGCTTTAAGTGTAAACAGTGCAGTTTGGTGGCTCTAAACAATGTCAAAGCTTCGACA	1425
Qy	402	AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly	421
Db	1426	ATAGTCTCTGGGAACACTGCTACGACAGATACCGGCTCAAAATGATCTGATTCAGT	1485
Qy	422	LysSerGluThrArgValGlnAsnGlyArgSer	432
Db	1486	AAGTCAGAGACTCGTGTCCAAACGTCGGTCC 1518	

RESULT 9

US-09-877-476-17

; Sequence 17, Application US/09877476

; Patent No. US20020049994A1

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.

; APPLICANT: Blacklock, Brenda J.

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09/877,476

; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,326

; PRIOR FILING DATE: 2000-06-08

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 1518

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 5' 222 bp from A. thaliana PAE1 (SEQ ID NO:1) and

; OTHER INFORMATION: 3' 1296 bp from B. napus elongase KCS (SEQ ID

; OTHER INFORMATION: NO:3) having a mutation at position 917;

; OTHER INFORMATION: designated At74 G306D; hypothetical

; NAME/KEY: CDS

; LOCATION: (1)...(1515)

US-09-877-476-17

Alignment Scores:

Pred. No.:	2,74e-258	Length:	1518
Score:	2201.50	Matches:	423
Percent Similarity:	98.84%	Conservative:	3
Best Local Similarity:	98.14%	Mismatches:	4
Query Match:	97.63%	Indels:	1
DB:	10	Gaps:	

SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-17 (1-1518)


```
Qy 102 ThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnPro 121
Db 526 ACCAAGTTAACCTTAAGATATAGGTATATCTGTGGTGAACATCAAGCATGTTAATCCA 585
Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuValArgSerAsnValArgSer 141
Db 586 ACTCCATCGCTCCGCGATGGTGGTTAACACTTTCAGCTCCGGAAGCAACGTAAGAGGC 645
Qy 142 PheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db 646 TTAACTTGGTGGCATGGTGTAGTGGCGGCTTATAGCATTCATGATAGCAAGGAC 705
Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
Db 706 TTGTTCATGTCCTCAAAAATACCATATGCTTGTGGTGAGCAGACAGAAATCATCTAT 765
Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
Db 766 AACATTTACGCTGGTGATATAGTCCATGATGCTTTCAAAATGCTTGTCCGTTGGT 825
Qy 202 GlyAlaAlaIleLeuSerAsnLysProGlyAspArgAtgSerLysTyrGluLeu 221
Db 826 GGGCCGCGCTATTGCTCTCAACAACCTGGAGATCGTAGACGCTCCAGTAGACGCTA 885
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 886 GTTCACACGGTTCCGAACGCATACCGGAGCTGAGCACAAGCTTTTCGTTGGTGCAACAA 945
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db 946 GGAGCAGTGAGNACGGCAAAATCGGAGTGNGTTGTCCAAAGGACATACCGGATGTTGCT 1005
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
Db 1006 GGTGCAACGGTTAAGAAAACATAGCAACGCTGGGTCGCTGATTCCTCCGTTAAGCGAG 1065
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
Db 1066 AAACCTCTTTTTCGTTACCTTCATGGCAAGAACTTTTCAAGATAAAAATCAAAACAT 1125
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArg 321
Db 1126 TACTACGCTCCGGATTCAAACTTGCTATTGACCATTTTGTATACATCCCGGAGGAGA 1185
Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db 1186 GCCGTGATTGATGCTGAGAGAAGAACCTAGCCCTAGCACCGCATCGATAGAGGCATCA 1245
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrTyrGluLeuAla 361
Db 1246 AGATCAACGTTACATAGATTTGGAACACTTTCATCTAGCTCAATATGGTATGAGTTGGCA 1305
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
Db 1306 TACATAGAACAAAGGAAGGATGAAGAAAGGTAATAAAGTTTGGCAGATTGCTTTAGGG 1365
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr 401
Db 1366 TCAGCGCTTAAAGTGTACAGTGCAGTTTGGTGCTCTTAAACATGTCAAAGCTTCGACA 1425
Qy 402 AsnSerProTrpGluHisCysLysIleAspArgTyrProValLysIleAspSerAspGly 421
Db 1426 AATAGTCTCTGGGAACACTGCATCGACAGATACCCGCTCAAAATGATTCTGATTCAGGT 1485
Qy 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1486 AAGTCAGAGACTCGTGTCTCAAAACGGTCGGTCC 1518
```

RESULT 11

US-09-877-476-25

; Sequence 25, Application US/09877476

; Patent No. US2002004999A1

```
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 519 bp from A. thaliana FAEL (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1002 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3); designated At173
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
; US-09-877-476-25

Alignment Scores:
Pred. No.: 2,65e-255 Length: 1521
Score: 2177.00 Matches: 419
Percent Similarity: 98.15% Conservative: 5
Best Local Similarity: 96.99% Mismatches: 8
Query Match: 96.54% Indels: 0
DB: 10 Gaps: 0
```

SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-25 (1-1521)

```
Qy 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSer 20
Db 223 AATCCGGTTATCTCGTGTGACTACTCGTGTATCTTCCRCGCCCACTCAAGGTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db 283 GTCTCTAAAGTCATGGATATTTTCTACCAAAATAGAAAGCTGATCTTCTTCACGGAAC 342
Qy 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
Db 343 GTGGCATGTGATGATCGCTCTCGCTCGATTTCCTGAGGAAGATTCAGAGCGCTCAGGT 402
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGGTGATGAGACGTACAGTCTCTGAGGGACTCATTCACGTACCCACCGGGAAGACTTTT 462
Qy 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCAGCGTCACGTGAAGACAGACAGAGAGGTATCATCGGTGCGCTCGAAATCTATTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyTyrLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAAGCTTAACCCCTAAAGATATAGGTATAGTATCTTGTGGTGAACCTCAAGCATGTTAAT 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCATCGCTCTCGCGATGGTTCGTTTAACTTTTCAAGCTCCGGAAGCAACGTAAGA 642
Qy 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACTTTGGTGGCATGGGTTGTAGTGGCGGCTTATAGCCATTTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTTCATGTCCTCAATAAAATACGATATGCTCTTGTGTCGAGCAGACAGAAATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGGTGATTAAGTTCATGATGTTTCATATTGCTTCCGCTGT 822
```

```

; OTHER INFORMATION: designated At173 G307D
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-39

Alignment Scores:
Pred. No.: 3,51e-255 Length: 1521
Score: 2176.00 Matches: 419
Percent Similarity: 98.15% Conservative: 5
Best Local Similarity: 96.99% Mismatches: 8
Query Match: 96.50% Indels: 0
DB: 10 Gaps: 0

SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-39 (1-1521)
QY 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProProHisCysArgValSer 20
DB 223 AATCCGGTTTATCTCGTTGACTACTCGTTGTTACCTTCCACCCACCGCATCTCAAGATTAGT 282
QY 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
DB 283 GTCCTCTAAAGTCATGGATATTTCTACCAATAAGAAAGCTGATACTTCTTCACGGAAC 342
QY 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
DB 343 GTGGCATGTGATGATCCGTCCTCGCTCGATTCTCTGAGGAAGATTCAAGAGCGGTTCAGGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPhe 80
DB 403 CTAGGTGATGAGACGTACAGTCTCTGAGGAGCATCTTCACTACCTACCCGCGGAGACTTTT 462
QY 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
DB 463 GCACGGTCACCTGAGACAGACAGAGAGGTATCATCGTGGCTCGAAATCTATTTCAG 522
QY 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
DB 523 AACACCAACGTTTAAACCTTAAGATATAGTATACCTTGTGTGAACCTCAAGCATGTTTAA 582
QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
DB 583 CCAACTCCATCGCTCTCCGCGATGCTGTTAAACACTTCAAGCTCCGGAAGCAACGTAAGA 642
QY 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspIleLys 160
DB 643 AGCTTTAACCTTGGTGGCAITGGTGTAGTCCGGCTTATAGCCATTGATCTAGCAAG 702
QY 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
DB 703 GACTTGTGTGATGTCATATAAAATACGTATGCTCTTGTGTGAGCAGACAGAAATCACT 762
QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
DB 763 TATAACATTTACGCTGCTGATATAAGTCCATGATGGTTTCAAAATGCTTTCCTCGTGT 822
QY 201 GlyGlyAlaAlaIleLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
DB 823 GGTGGGCGCCCTATTGTTGCTCTCCAAACAGCCTGGAGATCGTAGACGGTCCCAAGTACGAG 882
QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
DB 883 CTAGTTTACACCGGTTCCGAACGCATACCGGAGCTGACGACAAGTCTTTTTCGTTCGTCG 942
QY 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
DB 943 CAGGAGACGATGAGACCGCAAAATCGGAGTGTGTTGTCGAGGACATACCCGATGTT 1002
QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuProLeuSer 280
DB 1003 GCTGTGCAACGGTTTAAAGAAAAACATAGCAACGTTGGTCCGTTGATTTCTTCGCTTAAG 1062
QY 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLys 300
DB 1063 GAGAAACCTCTTTTTCGTTACCTTTCATGGCAAGAAACTTTTCAAGAGATAAAATCAAA 1122
QY 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
DB 1123 CATTACTACTCCCGGATTCAACTTGCTATTGACCATTTTGTATACATCGCGGAGGC 1182
QY 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
DB 1183 AGACCGCTGATTGATGCTAGAGAAGAACCTAGCCCTAGCACCGATGATGTAGAGGCA 1242
QY 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeu 360
DB 1243 TCAAGATCAACGTTACATAGATTTGGAAACACTTCATCTAGCTCAATATGTTATGAGTTG 1302
QY 361 AlaTyrIleGluAlaLysGlyArgMetLysGlyAsnLysValTrpGlnIleAlaLeu 380
DB 1303 GCATACATAGACAAAGAAAGAGGTGAAGAAGGTAAATAAGTTGGCAGATTGCTTTA 1362
QY 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer 400
DB 1363 GGGTCAGGCTTTAAGTGTAAACAGTGCAGTTTGGTGGCTTAAACAAATGTCAAAAGCTTCG 1422
QY 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
DB 1423 ACAAAATAGTCTTGGCAACACTGCATGCACAGATACCGGTCCTCAAAATGATCTGATCA 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
DB 1483 GGTAGTCAAGACTCGTGTCCMAAACGGTCGGTCC 1518

RESULT 12
US-09-877-476-39
; Sequence 39, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETONCYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and
; 3' 1002 bp from B. napus elongase KCS (SEQ ID
; NO:3) and having a mutation at position 920;
```

Db 1063 GAGAAACTTCTTTTTCGTTACCTTCATGGCGAAGAACTTTTCAAGAGATAAAATCAA 1122
Qy 301 H1STYrTyValProAspPheLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
Db 1123 CATTAAGTCTCCGGAATTCACAACTTGCTATTGACCACTTTTGTATACATGCGGAGGC 1182
Qy 321 ArgAlaValIleAspValLeuGlyAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGAGCCGCTGATTGATGCTCTAGAGAAGAACTTAGCCCTAGCACCGATCGATGAGAGCA 1242
Qy 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeu 360
Db 1243 TCRAAGTCAACGCTTACATAGATTTTGGAAACACTTCATCTAGCTCAATATGATGAGTTG 1302
Qy 361 AlaTyrIleGluAlaGlyArgMetIleGlyAsnLysValTyrPheIleAlaLeu 380
Db 1303 GCATACATAGAAAGCAAGGAAGGATGAAGAAAGGTAAATAAGTTTGGCAGATTGCTTTA 1362
Qy 381 GlySerGlyPheLysCysAsnSerAlaValTyrValAlaLeuAsnValLysAlaSer 400
Db 1363 GGGTCAGGCTTTAAGTGTAAACAGTGCAGTTTGGGTGGCTTAACAATGTCAAAAGCTTCG 1422
Qy 401 ThrAsnSerProTyrPheHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAAAATAGTCTTGGGAACACTGCTACAGATACCCGCTCAAAATGTATCTGATCA 1482
Qy 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAGTCAGAGACTCGTGTCCAAAACGGTCGGTCC 1518

RESULT 13

US-09-877-476-31
; Sequence 31, Application US/09877476
; Patent NO. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G..
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 1197 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO:3) and 3' 324 bp from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:1); designated Bn399
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-31

Alignment Scores:
Pred. No.: 8,32e-253 Length: 1521
Score: 2156.50 Matches: 413
Percent Similarity: 97.22% Conservative: 6
Best Local Similarity: 95.82% Mismatches: 11
Query Match: 95.63% Indels: 1
Gaps: 1
DB: 1

SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-31 (1-1521)

Qy 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerVal 21
Db 229 CCGGTTTACCTCGTTGAGTACTGCTACTCTCCACCAACGCGATGTGATCAAGATATC 288
Qy 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41

Db 289 TCCAGGTCATGGATATCTTTATCAAGTAAAGAACTGAT---CCTTCTCGGAACGGC 345
Qy 42 ThrCysAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
Db 346 ACGTGCATGACTCGCTGGCTTGACTTCTTGAGGAAGATTCAAGAAGGTTTCAGGTCTA 405
Qy 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProArgLysThrPheAla 81
Db 406 GCGATGAACACTCAGGGCCCGAGGGGCTGCTTCAGGTCTCCCGGAAGACTTTTGGG 465
Qy 82 AlaAlaArgGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
Db 466 GCGGCGCTGAAGAGACGGAGCAAGTTATCATTTGGTGCCTAGAAAATCTATTCAAGAAC 525
Qy 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
Db 526 ACCAAGTTTAAACCTTAAGATATAGGTATCTTGGTGAACCTCAGCATGTTTAAATCCA 585
Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
Db 586 ACTCCATCGCTCTCCGCGATGGTGTAAACACTTTCAAGCTCCGAAGCAACGTAAGAAGC 645
Qy 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db 646 TTTAACCTTGGTGCATGGGTTGTAGTCCGCGGTTTATAGCCATTGATCTAGCAAGGAC 705
Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
Db 706 TTGTTGCATGTCCATAAAATACGTATGCTCTTGGTGGAGCAGAGACATCACTTAT 765
Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
Db 766 AACATTACGCTGGTGATATAGTCCATGATGGTTTCAAAATTCCTTGTTCGTGGT 825
Qy 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 826 GGGGCGCTATTTTGTCTCCCAACAGCCTGGAGATCGTAGACGCTCAAGTAGAGACTA 885
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 886 GTTCACACGGTTCCGAACGCATACCGGAGCTGACGGCAAGTCTTTTCGTTGCTGCAACAA 945
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db 946 GGAGACGATGAGAACGCGCAAAATCGGAGTGAGTTGTCCAGGACATTAACCGATGTGCT 1005
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
Db 1006 GGTCAACGGTTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTCGTTAAGCGAG 1065
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
Db 1066 AACTTCTTTTTCGTTACCTTCATGGCAGAACTTAGGACTATCCCGCATCGATGTGGAGCATCT 1125
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
Db 1126 TACTACGTCCTCCGATTTCAAACTTGCCTATTGACCATTTTGTATACATGCCGGAGGCGA 1185
Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db 1186 GCGGTGATCGATGACTAGAGAAGAACTTAGGACTATCCCGCATCGATGTGGAGCATCT 1245
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeuAla 361
Db 1246 AGATCAACGTTACATAGATTGGGAATACTTCATCTAGCTCAATTTGGTATGAATAGCA 1305
Qy 362 TyrIleGluAlaGlyArgMetLysLysGlyAsnLysValTyrPheIleAlaLeuGly 381
Db 1306 TACATAGAGCAAGGGAAGATGAAGAAAGGGAATAAAGCTTGGCAGATGCTTTAGGA 1365
Qy 382 SerGlyPheLysCysAsnSerAlaValTyrValAlaLeuAsnValLysAlaSerThr 401

Db 1366 TCAGGTTTAAGTCTAATAGTCGGTTGGGTGGCTCTACGCAATGTCAAGGATCGGCA 1425
QY 402 AnSerProTrpGluHisCysLeuAspGlyValProValLysLeuAspSerGly 421
Db 1426 AATAGTCTTGGCAACATTCGATCATGATAGATATCGGTTAAATGATTCGTGATTCGA 1485
QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1486 AAGTCAAGAGACTCATGTCTCAAAACGGTCGGTCC 1518

RESULT 14

US-09-877-476-23
; Sequence 23, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 759 bp from B. napus elongase KCS (SEQ ID
; OTHER INFORMATION: NO.3); designated At254
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
US-09-877-476-23

Alignment Scores:
Pred. No.: 9,58e-253 Length: 1521
Score: 2156.00 Matches: 413
Percent Similarity: 97.92% Conservative: 10
Best Local Similarity: 95.60% Mismatches: 9
Query Match: 95.61% Indels: 0
DB: 10 Gaps: 0

SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-23 (1-1521)

QY 1 AnProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSer 20
Db 223 AATCGGTTTATCTCGTCTGACTACTCGTGTGTACCTCCACCACCGCATCTCAAAAGTTAGT 282
QY 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsn 40
Db 283 GTCTCTAAAGTCATGATATTCTTACCAATAAGAAAGCTGATACTTCTTCACGCAAC 342
QY 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnArgSerGly 60
Db 343 GTGGCATGTGATGATCCGTCCTCGCTCGATTCCTGAGGAAGATTCAGAGCGTTCAAGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProArgLysThrPhe 80
Db 403 CTAGGTGATGAGACGCTACAGTCTCGAGGGACTCATTCACGTACCACCGCGGAAGACTTTT 462
QY 81 AlaAlaLargGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCAGGTCACCTGAGACAGACAGAGAGGTATCATCGTCCGCTCGAAATCTATTTCGAG 522
QY 101 AnThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsn 120
Db 523 AACCAAAAGTTAACCTTAGAGAGATGATGATCTGTGGTGAAGTCAAGCATGTTTAAAT 582
QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140

Db 583 CCAACTCCTTCGGTATCCCGCTATGCTGTAACTATTCAAGCTCCGAAGCAACATCAAA 642
QY 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAATCTAGGAGGAATGGTTGTAGTCTGGTGTATTGGCTATGATTTGGCTAAA 702
QY 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTTCATGTTTCATAAAACACATTATGCTCTCGTGTGAGCAGACAGAACTACT 762
QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTTACGCTGGTGATAAATAGGTCCATGATGGTTTCAAAATTTGCTTCCGTT 822
QY 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGCGCTATTGCTCTCCAACAAGCTGGAGATCGTAGACGGTCCCAAGTACGAG 882
QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTCCACACGGTTCGAACGCATACCGGAGCTGACGGCAAGTCTTTTCGTGGCTCAA 942
QY 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGAGACGATGAGAACGGCAAAATCGGAGTGGTGTTCCTCAAGGACATAACCGATGT 1002
QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGGTCCGACGGTTAAGAAAAACATAGCAAGCTTGGTCCGTTGATTTCCGTTAAGC 1062
QY 281 GluLysLeuLeuPhePheValThrPheMetCysLysLysLeuPheLysAspLysLys 300
Db 1063 GGAACATCTCTTTTTCGTTTACCTTCATGGCAAGAACTTTTCAAGATATAAATCAA 1122
QY 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
Db 1123 CATTACTACGTCGGGATTTCAAACTTGCTATTGACCATTTTGTATACATGCGCGAGGC 1182
QY 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGAGCCGTGATTCATGCTGTAGAGAAGAACTAGCCCTAGCACCAGTCATGATAGGCA 1242
QY 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeu 360
Db 1243 TCAAGATCAACGTTACTAGATTGGAAACACTTCATCTAGCTCAATATGATGAGTTG 1302
QY 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
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QY 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer 400
Db 1363 GGGTCAGGCTTTAAGTGTAAACAGTCCAGTTGGGTGGCTCTAAACAATGTCAAAGCTTCG 1422
QY 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAAAATAGTCTTGGGAACACATGTCATCGACAGATACCGGTCAAAATTTGATTTCTGATCA 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAAGTCAGAGACTCGTGTCCCAAAACGGTCGGTCC 1518

RESULT 15

US-09-877-476-37
; Sequence 37, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001

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; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 762 bp from A. thaliana PAE1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 759 bp from B. napus elongase KCS (SEQ ID NO:3)
; OTHER INFORMATION: and having a mutation at position 920; designated
; OTHER INFORMATION: At254 G307D; hypothetical
; NAME/KEY: CDS
; LOCATION: (1)...(1518)
; US-09-877-476-37

Alignment Scores:
Pred. No.: 1 27e-252 Length: 1521
Score: 2155.00 Matches: 413
Percent Similarity: 97.92% Conservative: 10
Best Local Similarity: 95.60% Mismatches: 9
Query Match: 95.57% Indels: 0
DB: 10 Gaps: 0

SEQ12-JOIN-SEQ4 (1-432) x US-09-877-476-37 (1-1521)
QY 1 AsnProValThrLeuValAspThrSerCysTyrLeuProProHisCysArgValSer 20
DB 223 ATCCGGTTATCTCGTGTACTACTCGTGTACTCTCCACCACCGCATCTCAAGTTAGT 282
QY 21 ValSerValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
DB 283 GTCTCTAAGTCATGGATATTTCTACCAATAAAGAAAGCTGATATCTTCTTCACGGAAC 342
QY 41 GlyThrCysAspSerSerTrpLeuAspPheLeuArgLysIleGlnIleArgSerGly 60
DB 343 GTGGCATGTGATGCTCGCTCGATTTCTCGTGAAGATTTCAAGAGCGTTTCAGGT 402
QY 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProArgLysThrPhe 80
DB 403 CTAGGTGATGAGAGTACACTCTGAGGACCTCATTCACGTACCACCGCGGGAAGACTTTT 462
QY 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
DB 463 GCAGCGTCACGTGAAGACAGACAGAGAGTTATCATCGGTGCGCTCGGAAATCTATTCGAG 522
QY 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
DB 523 AACACCAAGTTAAACCTACAGAGATTTGTTACTTTGTTGAACCTCAAGCATGTTTAAT 582
QY 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
DB 583 CCNACTCTTCGCTATCCGTATGCTGTGTTACTTTCAAGCTCCGACGACACATCAAA 642
QY 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
DB 643 AGCTTTAATCTAGGAGGAATGGGTTGTTAGTGTGTTGTTATTCGCTATGTTGGCTAAA 702
QY 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
DB 703 GACTTGTGCTATTCATAAAACACTTATGCTCTGCTGTTGAGCAGACAGAAACATCACT 762
QY 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
DB 763 TATAACATTTACGCTGGTGATATAAGTCCATGATGGTTTCAAAATGCTGTGTTCCGTGTT 822
QY 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
DB 823 GTGGGGCGCGTATTTGCTCTCCAAACAGCCTGGAGATCTAGACGGTCCCAAGTACGAG 882
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```
QY 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
DB 883 CTAGTTTACACCGGTTTCAGCGCATACCGGAGCTGACGACAGCTCTTTTTCGTTCCGTCGAA 942
QY 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
DB 943 CAAGGAGACGATGAGAACGCGCAAAATCGGAGTGTGTTCCAAAGACATAACCGATGTT 1002
QY 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSer 280
DB 1003 GCTGTGTCACCGTTTAAAGAAAACATAGCAAGTTGGTCCGTTGATTCTTCGTTAAGC 1062
QY 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLys 300
DB 1063 GAGAAACTCTCTTTTTCGTTACCTTCATGGCGAAGAACTTTTCAAGATATAAATCAAA 1122
QY 301 HisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
DB 1123 CATTTACTAGTCCCGGATTTCAAACTTGCTATTGACCATTTTGTATACATGCCGAGGC 1182
QY 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
DB 1183 AGAGCGGTGATGATGTCTAGAGAAAGAACCTAGCCCTAGCAGCCGATCGATAGAGCA 1242
QY 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTrpTyrGluLeu 360
DB 1243 TCAAGATCAACGTTACATAGATTTTGGAAACACTTCATCTAGCTCAATATGTTAGTTG 1302
QY 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
DB 1303 GCATACATAGAAGCAAAAGGAGATGAAGAAAGTAAATAAGTTTGGCAGATTGCTTTA 1362
QY 381 GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSer 400
DB 1363 GGGTCAGGCTTTAAGTGTAAACAGTTCAGTTCAGTTGGTGGCTCTAAACAATGTCAAAGCTTCG 1422
QY 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
DB 1423 ACAAAATAGTCTCTGGGAACACTGCATCGACAGATACCGGTCGCTCTAAACAATGTCAAAGCTTCG 1482
QY 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
DB 1483 GGTNAGTCAGAGACTCGTGTCCAAAACGGTCGGTCC 1518
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Search completed: January 6, 2003, 20:28:54
Job time : 74.5 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2003, 16:29:00 ; Search time 1402 Seconds
(without alignments)
4990.335 Million cell updates/sec

Title: SEQ12-JOIN-SEQ4
Perfect score: 2255
Sequence: 1 NPVLVDVSYCLPPPHCRVS.....PVKIDSDSGKSETRVQNGRS 432

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QFMT=fastap SUFFIX=rst MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
-WARN_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: gb_est4.*
14: gb_est5.*
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16: em_estom.*
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20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_nam.*
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26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1102	52.4	1981	11	AY109713
c	1116.5	49.5	821	17	BH693376
3	1013.5	44.9	682	17	BH483730
c	993.5	44.1	1496	11	AY108343
5	982.5	43.6	915	14	BQ510080
6	936.5	41.5	765	14	BQ989474
c	934.5	41.4	801	17	BH696317
8	921.5	40.9	738	12	BG586676
9	915.5	40.6	755	14	BQ872186
10	910.5	40.4	770	14	BQ855453
11	888.5	39.4	735	12	BG599761
12	884.5	39.2	800	12	BG646966
13	882.5	39.1	769	17	BH512254
14	877.5	38.9	840	10	BE055710
15	871.5	38.6	867	13	BT949576
16	871	38.6	958	12	BG444087
c	866.5	38.4	806	17	BH460083
18	849.5	37.7	830	10	BE642815
19	847	37.6	912	12	BG837722
20	843	37.4	1086	17	BT13168
21	824.5	36.6	722	14	BQ012426
22	810.5	35.9	671	13	BJ281418
23	809.5	35.9	693	12	BG441374
24	808	35.8	864	12	BG444393
25	804.5	35.7	684	9	AL505481
26	802.5	35.6	727	13	BT422308
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28	790	35.0	662	14	BQ852310
29	789.5	35.0	663	14	BQ405604
30	785.5	34.8	715	14	BQ993166
31	781	34.6	680	14	BQ407349
32	768.5	34.1	669	12	BG441089
33	767.5	34.0	634	14	BQ245540
34	763.5	33.9	768	13	BT434568
35	761.5	33.8	685	12	BG443505
36	758	33.6	814	17	BH664493
37	756.5	33.5	715	12	BG128306
38	755.5	33.5	629	14	BQ801648
39	755	33.5	704	10	BE053446
40	754.5	33.5	642	13	BQ302152
41	749.5	33.2	753	12	BG123587
42	747.5	33.1	745	12	BG128875
43	746.5	33.1	641	12	BG442442
44	745	33.0	658	14	BQ407823
45	744.5	33.0	608	14	BQ629584

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Zea mays CL1191_1 mRNA sequence.
ACCESSION AY109713
VERSION AY109713.1 GI:21213540
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1981)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whittsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.


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  source      Location/Qualifiers
1..821
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  /strain="T01000DH3"
  /db_xref="taxon:3712"
  /clone_lib="BO_2_3_KB"
  /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT  198 a 203 c 185 g 235 t
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Alignment Scores:
Pred. No.:      3.82e-125      Length:      821
Score:          1116.50      Matches:    214
Percent Similarity: 88.97%      Conservative: 28
Best Local Similarity: 78.68%      Mismatches: 29
Query Match:    49.51%      Indels:     1
DB:             17          Gaps:         1
SEQ12-JOIN-SEQ4 (1-432) x BH693376 (1-821)
QY 104 ValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnProThrPro 123
Db 816 GTCCACCGCGGAGATCGTATAAATCATCTCAACTCAAGCAGCTTTAAACCGACTCCT 757
QY 124 SerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPheAsn 143
Db 756 TCGCTCTCAGCGAGTTGTGAACAAGTACAAAGCTCAGGACCAACATCAAAACATCAAT 697
QY 144 LeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeuLeu 163
Db 696 CTTGGCGGTATGGGCTGCACCGCAGCGCATTTGCCATCGATCTCGCAAGGACTTGTG 637
QY 164 HisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsnIle 183
Db 636 CAAGTCCATAAGAACACTTAGCTCTTGTGTGACGACAGATATACGCCGCCAACGG 577
QY 184 TyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGlyAla 203
Db 576 TACGACGTTGACAAATCAATGATGTGCGAAACTCTTGTGTCTAGTGGGGCC 517
QY 204 AlaIleLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuValHis 223
Db 516 GCGATATTTGCTCTCAAAACAAACGGGAGACAGGACGTTCCAAAGTATAAAGTCTCCAC 457
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Db 456 ACGGTTCCGACACACACGGGCGGATGACAAATCTTTAGATGTGTGCAACAAGAAGAT 397
QY 244 AspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGlyArg 263
Db 396 GATGACAAAGGCAAACTGGCATTTTCATTGACTAAAGACATAACCTCTGTGCTGGAGA 337
QY 264 ThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLysLeu 283
Db 336 ACCATTACCAAAACATAGCCACTTTGGTTCGTTGTTCTCCCGTGAGCGGAGAGCTC 277
QY 284 LeuPheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyrTyr 303
Db 276 CTGTTTTTCAAGACATATATACGAAGAAGTACTTCGACGACCAAGATTAAACAC---TAT 220
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Db 219 GTTCCGGATTTAAGCCTGCCATTGATCATTTCTGTATCCACCGGGTGGGAGAGCTCTG 160
QY 324 IleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArgSer 343
Db 159 ATCGATGAGCTCGGAAGAGGTTGGGGCTATCTCCGTTGACCTGGAGCCATCTAGATCA 100
QY 344 ThrLeuHisArgPheGlyAsnThrSerSerSerIleThrPyrGluLeuAlaTyrIle 363
Db 99 ACTTTGATAGGTTTGGTAACTCTCTCGAGATTCTATTGGTATGAGTTGGCTTATACG 40
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Db 39 GAGGCTAAAGGTAAAGAAAAAAGGGGACAAAGCTG 4
RESULT 3
LOCUS      BH483730
DEFINITION BOHAV15FP BOHA Brassica oleracea genomic clone BOHAV15, DNA
sequence.
VERSION    BH483730
KEYWORDS   BH483730.1 GI:17691834
SOURCE     GSS.
ORGANISM   Brassica oleracea.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 682)
TOWN,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOHAV15TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
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  source      Location/Qualifiers
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  /organism="Brassica oleracea"
  /strain="T01000DH3"
  /db_xref="taxon:3712"
  /clone_lib="BOHAV15"
  /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT  168 a 165 c 162 g 187 t
ORIGIN
Alignment Scores:
Pred. No.:      1.05e-112      Length:      682
Score:          1013.50      Matches:    201
Percent Similarity: 95.77%      Conservative: 3
Best Local Similarity: 94.37%      Mismatches: 8
Query Match:    44.94%      Indels:     2
DB:             17          Gaps:         1
SEQ12-JOIN-SEQ4 (1-432) x BH483730 (1-682)
QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerVal 21
Db 47 CCGGTTTACCTGCTGTGAGTACTCATGCTTACCACCAACGATTTAGATCAAGTATC 106
QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
Db 107 TCCAAGGTCATGGATATCTTTTACCAAGTAGAAGAGCTGAT---CCTTCTCGGAACGC 163
QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
Db 164 ACSTGGCATCACTCGCTCCCTGGCTTGACTTCTTGAGGAAGATTCAAGAAGCTTCAAGTCTA 223
QY 62 GlyAspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAla 81
Db 224 GCGCATGAACACCACCGCCCGGAGGCTGCTTCAGTCCCTCCCGGAAGACTTTTGG 283
QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
Db 284 GCGCGCGTGAAGAGACGAGCAGGATTATCATTTGGTGGCTAGAAAAATCTATTCAAGAAC 343
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QY 404 oTrrGluHisCysIleAspArgTyrProValLysIleAspSer 418
DB 412 CTGGCTGGACTGACGACAGTACCGCGGCGCATGGACGCC 370

RESULT 5
BQ510080
LOCUS BQ510080 915 bp mRNA linear EST 22-JUL-2002
DEFINITION EST617495 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMHH64 3' end mRNA sequence.
ACCESSION BQ510080
VERSION BQ510080.2 GI:21925787
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 915)
AUTHORS Buell C.R., Hart A., Baker B., Tanksley S., Fry W., Smart C., Restrepo S., Griffiths H., van der Hoeven R., Tsai J. and Karanymcheva S.A.
TITLE Generation of a set of potato cDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT On Jun 10, 2002 this sequence version replaced gi:21368949.
Other ESTs: EST617494
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatogr@tigr.org
This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or cdnatesgen.com
Seq primer: 77.

FEATURES
source
Location/Qualifiers
1..915
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjete"
/db_xref="taxon:4113"
/clone="STMHH64"
/clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site1: EcoRI; Site2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes tubers, or roots."
BASE COUNT 234 a 158 c 238 g 285 t
ORIGIN
BQ510080
Alignment Scores:
Pred. No.: 1,01e-108 Length: 915
Score: 982.50 Matches: 197
Percent Similarity: 78.93% Conservative: 39
Best Local Similarity: 65.89% Mismatches: 59
Query Match: 43.57% Indels: 4
DB: 14 Gaps: 3

SEQ12-JOIN-SEQ4 (1-432) x BQ510080 (1-915)
QY 37 SerSerArgAsnGlyThrCysAspAspSerSerTropLeuAspPheLeuArgGlyIleGln 56
DB 25 TCAGCGTCACCGGTGATTTGATGAGTCGCG---CTTGAGTTTCAGAGAAATCTG 81
QY 57 GluArgSerGlyLeuGlyAspGluThrHisGlyProGluGlyLeuGlnValProPro 76
DB 82 GAACGTTCTGGCCCTCGGGGACGAACTTATGTCCTCAGCTATCATCGCTCCCG 141
QY 77 ArgLysThrPheAlaAlaAlaArgGluThrGluGlnValIleIleGlyAlaLeuGlu 96

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DB 142 CAGCCTTCTATCCAGCGTCGCGAGAGAGCGCTGAGCAAGTTATGTTTGGCTACGGAC 201
QY 97 AsnLeuPheLysAsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSer 116
DB 202 AAATTTGTTTGCCTAATACCTCTGTGAACCTTAAGAAATAGGTGCTGTGTGAATGT 261
QY 117 SerMetPheAsnProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArg 136
DB 262 AGTTTGTCAATCCGACCTCCATCTTCAGCTATGATGATTGTAACAAGTATAAGTTGAGA 321
QY 137 SerAsnValArgSerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIle 156
DB 322 GGTAAATATAGGAGTTTAACTCGGGAGGTATGGGTGTAGTGGTGTAAATTCGGCT 381
QY 157 AspLeuAlaLysAspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThr 176
DB 382 GATCTTGCCAGAGCATGTTGCAAGTCACAGAAATACCTATGCTGTGTGTAGTACT 441
QY 177 GluAsnIleThrTyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCys 196
DB 442 GAGATATTACTCAGACTGCTATTTTGGGAATAGAAGTCCATGTTGATACCAATTT 501
QY 197 LeuPheArgValGlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgArg 216
DB 502 TTGTTTAGAGTCGGAGGTCTGCTGCTCTCTAAATAGCTATGATGATGAGAAGG 561
QY 217 SerLysTyrGluLeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPhe 236
DB 562 GCGAAATATAAGCTTGTTCATGCTGTAGGACACATCGTGGGGCTGATGATAAGCATTT 621
QY 237 ArgCysValGlnGlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAsp 256
DB 622 CGTGTGTTTACCAGACACAGATGATGCTGGGAAACCTGGGGTTCTTCTGTCAAAGAT 681
QY 257 IleThrAspValAlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIle 276
DB 682 CTCATGGCAATCGTGGGGAGCGCTTTAGACCAATATTACTACATGGGCTCTTGT 741
QY 277 LeuProLeuSerGluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLys 296
DB 742 CTACCCATCATGAGCAGCTGCTGTTCTGTTGTTCTCTGTAATCAAGAAATATTTAAT 801
QY 297 AspLysIleLysHisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIle 316
DB 802 AAGCATATCAGCT---TACATTCAGATTTCAGTTGGCCTTTGATCATTTCTGCATA 858
QY 317 HisAlaGlyGlyArgAla---ValIleAspValLeu-GluLysAsnLeuAlaLeu 333
DB 859 CACGCTGGGTGGGAGGGGTGCTGTTTTCAGCAGCTGGGAAAGAAATTTACAGCTG 913

RESULT 6
BQ989474
LOCUS BQ989474 765 bp mRNA linear EST 21-AUG-2002
DEFINITION QGF17M08.yg.abi.QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
ACCESSION BQ989474
VERSION BQ989474.1 GI:22409009
KEYWORDS EST.
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae; Lactuca.
REFERENCE 1 (bases 1 to 765)
AUTHORS Kozik A., Michelmore R.W., Knapp S., Matvienko M., Rieseberg L., Lin H., van Damme M., Lavelle D., Chevalier P., Ziegler J., Ellison P., Volkman J., Slabaugh M.S., Livingston K., Zhou Y., Lai Z., Church S., Jackson L. and Bradford K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
JOURNAL http://compgenomics.ucdavis.edu/
COMMENT Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]

```

Department of Vegetable Crops, R.W. Michelmore Lab
University of California at Davis (UCD)
Ammundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-742-9659
Email: akozlikeatgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig Q6_CA.Contig4873, see http://cgdb.ucdavis.edu/
for details.
Plate: QGF17 row: M column: 08.

FEATURES

Location/Qualifiers
1..765
/organism="Lactuca sativa"
/cultivar="L. serriola"
/db_xref="taxon:4236"
/clone="QGF17M08"
/clone_lib="Q6_EFGHJ lettuce serriola"
/lab_host="E. coli"
/note="Vector: pBRCDNASFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB-Q6_EFGHJ lettuce serriola
TAG_TISSUE-flowers pre-fertilized
TAG_SEQ-GCTTCACGGG"

BASE COUNT 219 a 182 c 163 g 201 t
ORIGIN

Alignment Scores:
Pred. No.: 3.13e-103 Length: 765
Score: 936.50 Matches: 181
Percent Similarity: 82.42% Conservative: 30
Best Local Similarity: 70.70% Mismatches: 44
Query Match: 41.53% Indels: 1
DB: 14 Gaps: 1

SEQ12-JOIN-SEQ4 (1-432) x B0989474 (1-765)

Qy 85 GluGluThrGluGluValIleGlyAlaLeuGluAsnLeuPheGlyAsnThrAsnVal 104
Db 1 GAGGAGCGGAGCGAGTGTAGCGAGCTTTAGATAATCTGTTTCCAGTACCGGAGT 60
Qy 105 AsnProLysAspIleGlyLeuValAsnSerSerMetPheAsnProThrProSer 124
Db 61 AAACCAAGACATCGGCATCTTGTGTGACTGTAGCTTGTTCATCCGACTCTTCC 120
Qy 125 LeuSerAlaMetValIleAsnThrPheLysLeuArgSerAsnValArgSerPheAsnLeu 144
Db 121 TTGTCTTCCATGATGTTAAACAAATACAAATTAAGAGGTAAATCCGAGCTTCAATTTG 180
Qy 145 GlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeuHis 164
Db 181 GCGGGAATGGATGCGAGCGCGGTGTGATGCCATCGATCGCCCAAGGATATGTTACAG 240
Qy 165 ValHisLysAsnThrTyrAlaLeuValIleSerThrGluAsnIleThrTyrAsnIleTyr 184
Db 241 GTTCACCGGAATACATACCGCGTGTGTGACGACCGAAACATCAACAAATTTGGTAT 300
Qy 185 AlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyAlaAla 204
Db 301 TTCGGGAACAAAAGATCCATGCTGATCCCAATTTTATTTATTCGAGTCGGTGTCTGCA 360
Qy 205 IleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuValHisThr 224
Db 361 GTTTTACTCTCCCAACAAATCAATCATGATAAAGACGACGAAATATACAAATCGTTCATGTC 420
Qy 225 ValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGlyAspAsp 244
Db 421 GTGAGAACCCACCGCGGTGCAGATGAGAAAGCTTTCCGTTGCGTATATCAAGAACAC 480

Qy 245 GluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGlyArgThr 264
Db 481 CCCGCCGAAAAAAGTGGTCTCTCTTTATCAAAAGATCTCATGCAATCGCGCGCGCA 540
Qy 265 ValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSerGlyLysLeu 284
Db 541 CTGAACCAACATCACTACTCTGGCCCATCTTCTTCCATCATGACGAGCTCCTT 600
Qy 285 PhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyrTyrVal 304
Db 601 TTCCTTCGCACCTTTAATAATAAAAAATTTCTTAATAACACATCAAAACC---TACATT 657
Qy 305 ProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArgAlaValIle 324
Db 658 CTGATTTCAAAATTAAGCTTTTCACCATCTTCGCATCCAGCTGGTGGTGGCTGTGATT 717
Qy 325 AspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 718 GATGAGCTTGAGAGAATCTGCAGCTATACCCGACATCTTGAAGCG 765

RESULT 7

BH696317/c BH696317 801 bp DNA linear GSS 20-FEB-2002
LOCUS BOM0247TF BO_2_3_KB Brassica oleracea genomic clone BOM0247, DNA
DEFINITION sequence.

ACCESSION BH696317
VERSION BH696317.1 GI:18768933
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea.

REFERENCE
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOM0247TR
Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..801
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOM0247"
/clone_lib="BO_2_3_KB"
/notes="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

FEATURES

BASE COUNT 235 a 198 c 150 g 218 t
ORIGIN
Alignment Scores:
Pred. No.: 5.9e-103 Length: 801
Score: 934.50 Matches: 178
Percent Similarity: 85.66% Conservative: 31
Best Local Similarity: 72.95% Mismatches: 34
Query Match: 41.44% Indels: 2
DB: 17 Gaps: 1

SEQ12-JOIN-SEQ4 (1-432) x BH696317 (1-801)

Qy 174 ValSerThrGluAsnIleThrTyrAsnIleTyrAlaGlyAspAsnArgSerMetMetVal 193
Db 799 GTGACCGGAGACATCACTCACTCAAGAACTG-TACTTAGGTAAACAACAAATCGATTGGTT 741

Alignment Scores: 2.11e-97 Length: 735
Pred. No.: 888.50 Matches: 171
Score: 88.50 Conservative: 32
Percent Similarity: 82.86% Mismatches: 41
Best Local Similarity: 69.80% Indels: 1
Query Match: 39.40% Gaps: 1
DB: 12

SEQ12-JOIN-SEQ4 (1-432) x BG599761 (1-735)

Qy 124 SerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPheAsn 143
Db 4 TCITTCGCCGATGATGTTATCATATATAACTTATGAGGGAATGTTATAGTACAT 63
Qy 144 LeuGlyGlyMetGlyCysSerAlaGlyValAlaAlaLeuAspLeuAlaLysAspLeuLeu 163
Db 64 CTTGGTGAATGGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 123
Qy 164 HisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsnIle 183
Db 124 CAAGTCCATCCACACATATGCTTGGTCTTAGTATGGAACATCATCTTGAATTGG 183
Qy 184 TyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyAla 203
Db 184 TATTTGGTAAATGAGAAATCCATGCTCTCCGAATGTTATTCGGATGGGGTGGCT 243
Qy 204 AlaIleLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuValHis 223
Db 244 GCTGTGCTCTCAATAAACGATCTGATAGGAACGATCAAGTACAGCTGGTCCAT 303
Qy 224 ThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlyAsp 243
Db 304 ACTGTAGAACTCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 363
Qy 244 AspGluAsnGlyLysIleValSerLeuSerLysAspIleThrAspValAlaGlyArg 263
Db 364 TATTCGGATGGAAGAGTGGGCTCTCTGTCAAAAGAGCTAATGGCAGTAGCTGGGAT 423
Qy 264 ThrValLysAsnIleAlaThrLeuGlyProLeuIleProLeuSerGluLysLeu 283
Db 424 GCTCTGAAGCAACATCAACATAGTGGTCTCTGCTTCCATGCTGAGCAATTC 483
Qy 284 LeuPhePheValThrPheMetGlyLysLeuPheLysAspLysIleLysHisTyrTyr 303
Db 484 CTTTTCCTCCACATTTGGTGGGAAGGCTATTGAAGGCGGAAGTAAGGCCT---TAT 540
Qy 304 ValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAlaVal 323
Db 541 ATCCCTGATTTTATGATAGTATGAGCATTTCTGCATTCATGCTGGTGGAGAGCTGTA 600
Qy 324 IleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArgSer 343
Db 601 CTGGATGAACATAGAAAACCTTCAGCTCTCTGATTTGGCATATGGAGCCTTCAGAA 660
Qy 344 ThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTyrTyrGluLeuAlaTyrIle 363
Db 661 ACATTCATCGATTGGCAACACTTCAAGCAGCTCCCTTTGGTACGAATGGCCTATTCG 720
Qy 364 GluAlaLysGlyArg 368
Db 721 GAAGCAAGGGTAGG 735

RESULT 12
LOCUS BG646966 800 bp mRNA linear EST 24-APR-2001
DEFINITION EST508585 HOGA Medicago truncatula cDNA clone phOGA-15E18 5' end,
mRNA sequence.
ACCESSION BG646966
VERSION BG646966.1 GI:13782078
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula

REFERENCE

AUTHORS Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
Utterback,T., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula treated with
oligogalacturonides of DP 6-20

JOURNAL

COMMENT Contact: Michael G. Hahn
Unpublished (2001)
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccrc.uga.edu

GS90572e RIGR sequence name: MTMBT33TK More information is
available at: www.medicago.org
Seq primer: SKmod (CTA gaa cta gta gAT CC).

FEATURES

source
1..800
/organism="Medicago truncatula"
/cultivar="A17"
/db_xref="taxon:3880"
/clone="phOGA-15E18"
/clone_lib="HOGA"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at 26 C
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in SOLR cells."

BASE COUNT 242 a 157 c 177 g 224 t

Alignment Scores:

Pred. No.: 7.42e-97 Length: 800
Score: 884.50 Matches: 171
Percent Similarity: 81.23% Conservative: 41
Best Local Similarity: 65.52% Mismatches: 47
Query Match: 39.22% Indels: 2
DB: 12 Gaps: 1

SEQ12-JOIN-SEQ4 (1-432) x BG646966 (1-800)

Qy 72 LeuGlnValProProArgLysThrPhe-AlaAlaAlaArgGluGluThrGluGlnValI 91
Db 2 ATGAGGGTCCCACTAAATCCATGATGGCTGAGCAAGGAAGAAGCTGAAGAGGTAT 61
Qy 91 eileGlyAlaLeuGluAsnLeuPheLysAsnThrAsnValAsnProLysAspIleGlyI 111
Db 62 GTTGGTGTCTATGATGAGGTCTTCAAAAACTGTGTGAAGGCTAAGGATATTGGAT 121
Qy 111 eLeuValValAsnSerSerMetPheAsnProThrProSerLeuSerAlaMetValValAs 131
Db 122 TTTGGTGTGGAATGATGTTGTTTATCCACACCATCTCTTTCTGCCATGATGTGAA 181
Qy 131 nThrPheLysLeuArgSerAsnValArgSerPheAsnLeuGlyGlyMetGlyCysSerAl 151
Db 182 TCATTATAGTTGAGAGGAATATCTTGATATATCTTTGGTGTATGGGTGTAGTGC 241
Qy 151 aGlyValIleAlaIleAspLeuLysAspLeuHisValHisLysAsnThrTyrAl 171
Db 242 TGCTCTTATCTATTGACCTTGCCAAACAGCTCTTACAGGTACATCCAAACTCATATGC 301
Qy 171 aLeuValValSerThrGluAsnIleThrTyrAsnIleThrTyrAlaGlyAspAsnArgSerMe 191

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

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|||||
302 CTTAGTAGTGAGCATGGAGAACATAACACTAACTGGTATTTCGGCAACGACAGATCAAT 361
Qy 191 tMetValSerAsnCysLeuPheArgValGlyGlyAlaIleLeuLeuSerAsnLysPr 211
|:|||||
362 GCTAGTGCCAAATGTTCTTTAGATGGGAGGAGCAGCAGTCTCTCCACACGCC 421
Qy 211 oGlyAspArgArgSerLysTyrGluLeuValHisThrValArgThrHisThrGlyAl 231
|:|||||
422 ACGGACCGCTCCGGATCAAAATACCAACTAGTCCACACCGCTCCGACACCAAGAGTGC 481
Qy 231 aAspGlyLysSerPheArgCysValGlnGlnGlyAspAspGluAsnGlyLysIleGlyVa 251
|:|||||
482 AGACACAAATCTTACGCTCGCTCTTCAAGAAGAACGACACACAAAGTCGGTGT 541
Qy 251 lSerLeuSerLysAspIleThrAspValAlaGlyArgThrValLysLysAsnIleAlaTh 271
|:|||||
542 ATCACTCTCAAAAGACCTAATGCTGTGCGGGAAGACACTCAAAACAAACATCACAC 601
Qy 271 rLeuGlyProLeuLeuProLeuSerGluLysLeuLeuPhePheValThrPheMetG1 291
|:|||||
602 ATTAGGACCAATTAGTCTTACCTATGTCGGAACAGCTCTATTATTTTCGGGACATGTTG 661
Qy 291 yLysLysLeuPheLysAspLysIleLysHisTyrTyrValProAspPheLysLeuAla1 311
|:|||||
662 GCGAAATCTTCAAGATGAATNAACCA--TACATCTCTGATTTTAAATAGCTTT 718
Qy 311 eAspHisPheCysIleHisAlaGlyGlyArgAlaValIleAspValLeuGluLysAsnLe 331
|:|||||
719 TGAGCATTTTGTATTATCATGCTGTGTGAAGAGCCTGTTTGGATGAGTGGAGAAATCTT 778
Qy 331 u 331
|
Db 779 G 779

RESULT 13
BH512254
LOCUS BOHKU08TF BOHK Brassica oleracea genomic clone BOHKU08, DNA
DEFINITION sequence.
ACCESSION BH512254
VERSION BH512254.1 GI:17720344
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea.
REFERENCE Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
AUTHORS Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOHKU08TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
FEATURES
Location/Qualifiers
source 1..769
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOHKU08"
/clone_lib="BOHK"
/note="vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT 195 a 204 c 159 g 211 t
ORIGIN

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Alignment Scores:
Pred. No.: 1..22e-96 Length: 769
Score: 882.50 Matches: 171
Percent Similarity: 97.21% Conserv: 3
Best Local Similarity: 95.53% Mismatches: 4
Query Match: 39.14% Indels: 1
DB: 17 Gaps: 1

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SEQ12-JOIN-SBQ4 (1-432) x BH512254 (1-769)

```

Qy 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerVal 21
|:|||||
Db 236 CCGGTTTACCTCGTGGTACTCATGCTACCTCCACCAACGATTGTAGATCAAGTATC 295
Qy 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
|:|||||
Db 296 TCCAAGGTCATGGATATCTTTTACCAGTAAGAAAGCTGAT---CCTTCTCGGAACGGC 352
Qy 42 ThrCysAspAspSerSerTyrLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
|:|||||
Db 353 ACCTGCGATGACTCTCTCGCTTGACTTCTTGAGGAAGATTCAAGAACGTTTCAGTCTA 412
Qy 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
|:|||||
Db 413 GCGCATGAACCCACGCGCGGAGGCTGCTTCAGTCCCTCCCGAAGACTTTTGGC 472
Qy 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
|:|||||
Db 473 GCGCGCGTGAAGAGACGCGAGGTTATCTNTGTCGCTAGAAAATCTATTCAAGAAC 532
Qy 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
|:|||||
Db 533 ACCAATGTTAACCTTACAGATATAGTATACCTTGTGTTGAACCTCAAGCATGTTTATCCA 592
Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
|:|||||
Db 593 ACCTCTTCGCTCTCCGCGATGGTGTAACTTCAAGCTCCGGAACACGTAAGAACG 652
Qy 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
|:|||||
Db 653 TTTAACTTGTGGCATGGTGTAGTCCGCGCTTATAGCCATTGATAGCAAAAGGAC 712
Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
|:|||||
Db 713 TTGTTGCATGTCCTCAAAAATACGATGCTCTTGTGTCGACGACAGAACATCACT 769

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```

BE055710 840 bp mRNA linear EST 07-MAR-2001
GA_Ea0035J01f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0035J01f, mRNA sequence.
ACCESSION BE055710
VERSION BE055710.2 GI:13246847
KEYWORDS EST
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.

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```

REFERENCE 1 (bases 1 to 840)
AUTHORS W.D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE An integrated analysis of the genetics, development, and evolution
JOURNAL of the cotton fiber
COMMENT Unpublished (2000)
On Jun 8, 2000 this sequence version replaced gi:8382767.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

```

Email: rwing@clermson.edu
Seq primer: TAATACGACTCATATAGGG
High quality sequence stop: 659.

FEATURES

source
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/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
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/clone_lib="GA_Ea0035701f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="fibers isolated from bolls harvested 7-10 dpa"
/lab_host="E. coli"
/note="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 238 a 173 c 198 g 229 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 5,73e-96 Length: 840
Score: 877.50 Matches: 187
Percent Similarity: 78.87% Conservative: 37
Best Local Similarity: 65.85% Mismatches: 56
Query Match: 38.91% Indels: 7
DB: 10 Gaps: 2

SEQ12-JOIN-SEQ4 (1-432) x BE055710 (1-840)

QY 104 ValAsnProGlyAspIleGlyLeuValValAsnSerSerMetPheAsnProThrPro 123
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QY 124 SerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPheAsn 143
Db 61 TCCTTGTCTGCCATGGTTATCAACCATTAACAGCTTCGAGGGAATATTCAAGCTACAA 120
QY 144 LeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeuLeu 163
Db 121 TTGGGAGGAGTGGCTGTAGTGGTGTCTCAATAGATCTTGCAAGAAATCTACTT 180
QY 164 HisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsnIle 193
Db 181 CAAGTCCATCCCAAGCTCTATGCATCGATTATCAGCATGGCAACATCACCTTGAACGTG 240
QY 184 TyrAlaGlyAspAsnArgSerMetValSerAsnCysLeuPheArgValGlyGlyAla 203
Db 241 TACTTTGGAATGATCGCTCAAACTTGTTCAACTGCTTATTCAGGATGGGAGCGCG 300
QY 204 AlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuValHis 223
Db 301 GCAATACCTCTCTAAACAACGCTCTGCACAGAAGAATCCAAATACCAATTTGGTTCAC 360
QY 224 ThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGlyAsp 243
Db 361 ACTGTTCCGACTCACAAAGCGCGGATGATAAGTGTCTTGTGTACACAGGAAGAA 420
QY 244 AspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGlyArg 263
Db 421 GACTCTGCAGAAAGATTTGGGCTTATCATGTTCAAAGATCTCATGCGAGTTCGGTGGAT 480
QY 264 ThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLysLeu 283
Db 481 GCTTAAAGACCAACATCACCATTCAGCATTTGGGGCTGTGGTTCGATGCTGAGCAGCT 540
QY 284 LeuPhePheValThr-PheMetGlyLysLysLeuPheLysAspLysIleLysHisTyrTy 303
Db 541 CTNTCTTCTCTACATTTGGTGGGAAGAGCTTATCANNATGACAGATCAAGCCT--TA 597
QY 303 rVal-ProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAlay 323
Db 598 CATTTCCAGATTTCAAGCTAGCTTTTGAACATTTCTGCATTCACGCTGGAGGAAGAACTG 657
QY 323 alIleAspValLeuGlyLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 343

Db 658 TTTTGTGATGAACCTGGAGAAGATTTCAGCTCTCCCAATGGCATATGGAAACCATCAAAA 717
QY 343 erThrLeuHisArgPheGlyAsnThrSerSerSerIleTrpTyrGluLeuAlaTyrI 363
Db 718 TGACTCTCTT-CGAATTGGAAAA---CCTCAAGCCAGCTCTCTGGGTATCAATGGGCTATC 773
QY 363 leGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGlySerG 383
Db 774 CGGAGAGCTTAGGGAGGATTAGGAAGGAACGAAC-CGCAAAA-GCATTTGGGTCTGT 831
QY 383 LypPheLys 385
Db 832 CATTCAAA 839

RESULT 15
BI949576
LOCUS
DEFINITION
BI949576 867 bp mRNA linear EST 19-OCT-2001
(HVSME100141L13f Hordeum vulgare spike EST library HVCNDA0012
Hordeum vulgare cDNA clone HVSME100141L13f, mRNA
sequence.)

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BI949576
BI949576
EST
Hordeum vulgare.
Hordeum vulgare.

REFERENCE
AUTHORS
1 (Bases 1 to 867)
; Triticaceae; Hordeum.

Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource for barley genomics: Fusarium infected Morex spike cDNA library Unpublished (2001)

Contact: Wing RA
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu

Total hq bases = 555
Seq primer: AATTACCCCTCACTAAAGG
High quality sequence stop: 610.

FEATURES

Source

1..867
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone_lib="HVSME100141L13f"
/clone_lib="Hordeum vulgare spike EST library HVCNDA0012 (Fusarium infected)"
/tissue_type="Spike"
/lab_host="TJCI21"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).

The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see

<http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wang R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/gpages/bgn/31/cover.html>)

BASE COUNT 200 a 223 c 260 g 182 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 3.25e-95 Length: 867
Score: 871.50 Matches: 188
Percent Similarity: 80.36% Conservative: 33
Best Local Similarity: 68.36% Mismatches: 53
Query Match: 38.65% Indels: 6
DB: 13 Gaps: 1

SEQ12-JOIN-SEQ4 (1-432) x BI949576 (1-867)

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Db 2 TTCACCGGACGGCGTCACTGTCGCCCATGGTGTGAACCATTAACAGCTGAGAGGAAC 61
QY 139 ValArgSerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeu 158
Db 62 ATAATCAGCTACAATCTGGGAGGAATGGGTGCGAGTCCGGGCTCTTCCATAGATCTG 121
QY 159 AlalysAspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsn 178
Db 122 GCCAAGGATTGCTTCAGGTGATCCCACTCGTACGCCATGGTGTGAGCAGCCGAGAAC 181
QY 179 IleThrTyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPhe 198
Db 182 ATTACCCGTGAATGGTATTTGGGAACAACCGGTGATGCTGTGCGAATGGCTGTTTC 241
QY 199 ArgValGlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLys 218
Db 242 CGGATGGTTCGCGTCGATCCTGCTGCGAACAAGCGGTCAACAGGAGGAGGTCCAAG 301
QY 219 TyrGluLeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCys 238
Db 302 TACGAGCTGTACACACCTGAGACTCACAAGGTCAGATGACAGTGTTCAGCTGT 361
QY 239 ValGlnGlnGlyAspAspGluAsnGlyLysIleGlyValSerLysSerLysAspIleThr 258
Db 362 GTCACCCAGGAGGAGGATCACAGTGGCAAGGTTGGCGTCGACATGTCCCAAGGACCTCATG 421
QY 259 AspValAlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProIleLeuPro 278
Db 422 CGGGTGGCTGGGATGCGCTCAAGACGAACATCAACCGTTGGCGCGCTTGTGTGCCA 481
QY 279 LeuSerGluLysLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLys 298
Db 482 TTCGCGAGCAGCTGCTGTTCAATGGTGTGGCAAGAGCTGTTCAGATGAAG 541
QY 299 IleLysHisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAla 318
Db 542 ATCAAGCCA--TACATTCCTCACTCAAGCTGGCATTCGAGCAGTTCGATCCAGCT 598
QY 319 GlyGlyArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspVal 338
Db 599 GGTGGCGCGCTGTGCTGTGATGAGATGAGAAGAC-ATGGACCTCACCGATGGCACATG 657
QY 339 GluAlaSerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrPyr 358
Db 658 GAGCCGCTCGGGGAGCTCTCTCCCG-TTCGGCAACACAGTCCACAGCTCGGTGGTAC 716
QY 359 GluLeuAlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpIle 378
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Db 717 AG-CTGCGCTTACACGACCCACAAAGGAGGAGGAGCCAGGAGCGGTATGGCAATA- 774

QY 379 AlalaLeuGlySerGlyPheLysCysAsnSerAlaValTrpValAla 393

Db 775 GCGNTCGGCTCGGGGTTCAA-TGTACAAGCGCGCTCTGGACGGCC 818

Search completed: January 6, 2003, 18:56:28
Job time : 1409 secs

GenCore version 5.1.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 6, 2003, 16:29:00 ; Search time 1402 Seconds
(without alignments)
4990.335 Million cell updates/sec

Title: SEQ14-JOIN-SEQ4
Perfect score: 2250
Sequence: 1 NPVYLVDYSCVLPPLPHLRVS.....PVKIDSDSGKSETRVONGRS 432

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=EST -QFW=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=diagsum2 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=MCELMAIN9877476.ecn_1.1573_runat_06012003_124916_33 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: em_estha.*
2: em_esthum.*
3: em_estlin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_nam.*
24: em_gss_nus.*
25: em_gss_othr.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	1183	52.6	1981	11	AY109713 Zea mays
c	1116.5	49.6	821	17	BH693376 BORHUS43TR
3	1003.5	44.6	682	17	BH483730 BORHUS15TF
c	993.5	44.2	1496	11	AY108343 Zea mays
5	982.5	43.7	915	14	BQ510080 EST617495
6	936.5	41.6	765	14	BQ510080 EST617495
c	934.5	41.5	801	17	BH696317 BOMQZ47TF
7	921.5	41.0	738	12	BH696317 BOMQZ47TF
8	915.5	40.7	755	14	BQ872186 QG113006
9	910.5	40.5	770	14	BQ872186 QG113006
10	885.5	39.5	735	12	BQ855453 QGB26K03
11	884.5	39.3	800	12	BQ855453 QGB26K03
12	877.5	39.0	840	10	BG546966 EST504656
13	872.5	38.8	769	17	BH512254 GA_Ea003
14	871.5	38.7	867	13	BH512254 GA_Ea003
15	871.5	38.7	867	13	BH512254 GA_Ea003
16	866.5	38.5	806	17	BH440087 HVSME1001
c	849.5	37.8	830	10	BH440087 HVSME1001
18	847	37.6	912	12	BH440087 HVSME1001
19	843	37.5	1086	17	BH440087 HVSME1001
20	824.5	36.6	722	14	BH440087 HVSME1001
21	824.5	36.6	722	14	BH440087 HVSME1001
22	810.5	36.0	671	13	BH440087 HVSME1001
23	809.5	36.0	693	12	BH440087 HVSME1001
24	808	35.9	864	12	BH440087 HVSME1001
25	804.5	35.8	684	9	AL505481
26	802.5	35.7	727	13	AL505481
27	791.5	35.2	665	17	BH560982
28	790	35.1	662	14	BH560982
29	789.5	35.1	663	14	BH560982
30	785.5	34.9	715	14	BQ933166
31	781	34.7	680	14	BQ933166
32	768.5	34.2	669	12	BG441089
33	767.5	34.1	634	14	BQ245540
34	763.5	33.9	768	13	BQ245540
35	761.5	33.8	685	12	BQ443505
36	758	33.7	814	17	BH664493
37	756.5	33.6	715	12	BH664493
38	755.5	33.6	629	14	BQ801648
39	755	33.6	704	10	BE053446
40	754.5	33.5	642	13	BH302152
41	749.5	33.3	753	12	BH302152
42	747.5	33.2	745	12	BH302152
43	746.5	33.2	641	12	BH302152
44	745	33.1	658	14	BQ407823
45	744.5	33.1	608	14	BQ629584

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Zea mays CL1191_1 mRNA sequence.
ACCESSION AY109713
VERSION AY109713.1 GI:21213540
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1981)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.


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FEATURES
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/db_xref="taxon:3712"
/clone_lib="BOHUS43"
/clone_lib="BO_2_3_KB"
/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT 198 a 203 c 185 g 235 t
ORIGIN
Alignment Scores:
Pred. No.:      8,9e-127      Length:      821
Score:          1116.50      Matches:     214
Percent Similarity: 88.97%      Conservative: 28
Best Local Similarity: 78.68%      Mismatches:  29
Query Match:    49.62%      Indels:      1
DB:             17          Gaps:         1

SEQ14-JOIN-SEQ4 (1-432) x BH693376 (1-821)
QY 104 ValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnProThrPro 123
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DB 816 GTCCACCGCGGAGATCGTATAATCATCTCACTCAAGCAGCGTTTAAACCGACTCCT 757
QY 124 SerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPheAsn 143
|||
DB 756 TCCTCTCAGCGATGGTGTGAACAAGTACAAAGCTCAGGAGCAACATCAAAAGCATCAAT 697
QY 144 LeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeuLeu 163
|||
DB 696 CTTGGCGGTATGGCTGCAGCGAGCGGTCACTGCCATCGATCTGCCAAAGGACTGTG 637
QY 164 HisValHisLysAsnThrThrAlaLeuValValSerThrGluAsnIleThrThrAsnIle 183
|||
DB 636 CAAGTCCATAGAACAACCTACGCTCTGTGGTGAGCAGACAGATATCAAGCAACGCG 577
QY 184 TyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGlyAla 203
|||
DB 576 TACGAGGTGCACAAACAATCAATGATGTGCGCAAACTGCTGTGCTAGTGGGGCC 517
QY 204 AlaIleLeuSerAsnLysProGlyAspArgArgSerLysThrGluLeuValHis 223
|||
DB 516 GCGATATTGCTCTCAACAACCGGAGCAGGAGAGCTTCCAGATATAAAGTCTCCAC 457
QY 224 ThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGlyAsp 243
|||
DB 456 ACGGTTCGGACACACACGGGAGCGGATGACAAATCTTTAGATGTGTGCAACAAGAAT 397
QY 244 AspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGlyArg 263
|||
DB 396 GATGACAGGGCAAAACTGGCATTCATGTACTAAAGACATACCTCTGTCTGGGAGA 337
QY 264 ThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLysLeu 283
|||
DB 336 ACCATTACCAAAAACATAGCCACTTTGGGTGCTGTTGTTCTCCCGGTGAGCGAGAAGCTC 277
QY 284 LeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysLysIleHisThrThr 303
|||
DB 276 CTGTTTTTCAAGACATATATACGCAAGAAGTACTTCGACACACAGATTAACAC---TAT 220
QY 304 ValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAlaVal 323
|||
DB 219 GTTCGGGATTTAAGCGGTGCCATTGATCATTTCTGTATCCACGCGGGTGGGAGAGCTCTG 160
QY 324 IleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArgSer 343
|||
DB 159 ATCGATGAGCTCGGGAAGAGGTGGGGCTATCTCCGGTTCACGTGGAGCCATCTAGATCA 100
QY 344 ThrLeuHisArgPheGlyAsnThrSerSerSerIleThrPyrGluLeuAlaThrIle 363
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DB 99 ACTTTGCATAGGTTGGTAATACTCTTCGAGTTCTATTGTTGGTATGAGTTGGCTTATACG 40

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QY 364 GluAlaLysGlyArgMetLysLysGlyAsnLysVal 375
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DB 39 GAGCTTAAGGTAAAGAAAAAAGGGGACAAAGCTG 4

RESULT 3
BH483730
LOCUS      BH483730
DEFINITION BOHAV15TF BOHA Brassica oleracea genomic clone BOHAV15, DNA
sequence.
ACCESSION  BH483730
VERSION    BH483730.1
KEYWORDS   GI:17691834
SOURCE     GSS.
ORGANISM   Brassica oleracea.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 682)
            Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
            Whole genome shotgun sequencing of Brassica oleracea
            Unpublished (2001)
            Other_GSSs: BOHAV15TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES
            source
            location/Qualifiers
            1..682
            /organism="Brassica oleracea"
            /strain="TO1000DH3"
            /db_xref="taxon:3712"
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            /clone_lib="BOHA"
            /note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
            genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT 168 a 165 c 162 g 187 t
ORIGIN
Alignment Scores:
Pred. No.:      5,94e-113      Length:      682
Score:          1003.50      Matches:     200
Percent Similarity: 95.31%      Conservative: 3
Best Local Similarity: 93.90%      Mismatches:  9
Query Match:    44.60%      Indels:      2
DB:             17          Gaps:         1

SEQ14-JOIN-SEQ4 (1-432) x BH483730 (1-682)
QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
|||||
DB 47 CCGGTTTACCTCGTTGAGTACTCATGTACTCTCCACCAACCAITGTAGATCAAGTATC 106
QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
|||||
DB 107 TCCAAGGTCAATGGATATCTTTTACCAAGTAGAAGAAAGCTGAT---CCTTCTCGGAAGCGC 163
QY 42 ThrCysAspAspSerSerTyrPheLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
|||||
DB 164 ACGTGGGATGACTCTGCTCGCTGGCTTGTACTCTTTCAGGAAGATTCAGAGCTCTA 223
QY 62 GlyAspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAla 81
|||||
DB 224 GGGGATGAACCAACACGCGGCGCGAGGGGCTGCTTTCAGGTCCCTCCCGGAGAGCTTTTGG 283
QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
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DB 284 GCGGCGGTGAAGAGACGAGCAGGAGTTTATCATTTGGTGGCTAGAGAAATCTATTCAAGAAC 343

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QY 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
Db 344 ACCAATGTTAAACCTTACAGATATAGGTATAGTGTGGTGAACCTCAAGCATGTTTAAATCCA 403

QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
Db 404 ACTCCTTCCTCCCGATGGCTGTTAACACTTTCAGCTCCGAGCAGCAAGCTTAAGAACG 463

QY 142 PheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
Db 464 TTTAACTTGGTGGCATGGTGTAGTGGCGGCTTATAGCAATGATCTAGCAAAAGGAC 523

QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
Db 524 TTGTTGCATGTCCTCAAAATACGATGCTCTGTGGTGAGCAGACAGACATCATCTAT 583

QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
Db 584 AACATTTAGCGTGGTGATAATAGTCCATGATGGTTTCAAAATGCTTTCCCGTGTGGT 643

QY 202 GlyAlaAlaIleLeuSerAsnLysProGlyAspArg 214
Db 644 GGGCGCGCTATTTTCTCTC-AACAAGCCTAGAGATCGT 681

RESULT 4
AY108343/c 1496 bp mRNA linear HTC 25-MAY-2002
LOCUS Zea mays PC0065510 mRNA sequence.
DEFINITION AY108343
ACCESSION AY108343
VERSION AY108343.1 GI:21211421
KEYWORDS HTC
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1496)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Zea Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1496)
AUTHORS Coe, E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES
source
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/organism="Zea mays"
/db_xref="MaizeDB:633522"
/db_xref="taxon:4577"
/clone="PC0065510"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/note="This sequence is part of a project of EST
assemblies resulting from the application of public
configs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT 277 a 455 c 503 g 261 t
ORIGIN

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Alignment Scores:

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Pred No.: 3 6e-111 Length: 1496
Score: 293.50 Matches: 193
Percent Similarity: 68.00% Conservativeness: 62
Best Local Similarity: 51.47% Mismatches: 100
Query Match: 44.16% Indels: 20
DB: 11 Gaps: 3

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SEQ014-JOIN-SEQ4 (1-432) x AY108343 (1-1496)
QY 62 GlyAspGluThrHisGlyProGlyLeuGluValProArgLysThrPheAla 81
Db 1486 GGCAGCAGTGTACATGCGCGCTGCTGTCGAG-----CCCAACGCCAGCTGCC 1433

QY 82 Ala-----AlaArgGluGluThrGluGluValIleIleGlyAlaLeuGluAsnLeu 98
Db 1432 ACCATGAAGGATGGCGCGCCGAGCGCTCCAGCGCCATGTCGCGCGCTGAGAGCTG 1373

QY 99 PheLysAsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerMet 118
Db 1372 TTTCGACAGTGGCGCGCTCCGCGCCAGGACGTGGCGCTGCTGCTCAACTGCAGCCTC 1313

QY 119 PheAsnProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsn 138
Db 1312 TTCACCGGACGCCCTCCCTGTCGCCATGATCGTCAACCACTACAGATGCGCGGCAC 1253

QY 139 ValArgSerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeu 158
Db 1252 ATCTCTGAGCTACAACTGGGGGCATGGCTGCAGCGCGCGCTCATCGCATCGACCTG 1193

QY 159 AlaLysAspLeuLeuHisValHis-LysAsnThrTyrAlaLeuValValSerThrGluAs 178
Db 1192 GCGCGCGACATGCTCCAGCGCGCGCTGGCGCTGGCGCTGGTGGTCCAGCAGGAGC 1133

QY 178 nIleThrTyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPh 198
Db 1132 CGTCTCTTACGCTGAGTACCGCGGGAAGCGGCTGCTCATCTCCCGAACGCCCTTCT 1073

QY 198 eArgValGlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLys 218
Db 1072 CCGGCGCGCTGGCGCGGCTGCTGTCCACCGCGCGCGGACTTCCACCGCGCCAA 1013

QY 218 sTyrGluLeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgC 238
Db 1012 GTACCAGCTGGAGCAGCTGGTGGCGCACACAGGCGCGGCGCGCTTCCGCTG 953

QY 238 sValGlnGlnLysAspGluAsnGlyLysIleGlyValSerLysSerLysAspIleTh 258
Db 952 CGTGATCCAGGAGGAGCAGCAGCGGATCAAGGCGCTGTCCATCAGCGCGGACCTGCT 893

QY 258 rAspValAlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuPr 278
Db 892 GGAGTGGGCGGCGCGCGCTCAAGACCAACATCACCACCGTGGGCGCGCTGCTGCC 833

QY 278 oLeuSerGluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAsp 298
Db 832 CTTCCTCCGAGCAGCTGCTCTTCTTCGCGGCGTGTGTTCCGCGACCTGTTCCCGTCCA 773

QY 298 s-----IleLysHisTyrTyrVa 304
Db 772 GCGCTGACGCGCGCGCGCGCGCCAGCCAGGAGGAGCGCTCGGCGCGCGCGCTTACAT 713

QY 304 lProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyLysValAlaVal 324
Db 712 CCGGACTTCAAGCGCGCTTCGAGCAGCTTCTGATGACGCGCGCGCGCGCGCTGCT 653

QY 324 eAspValLeuLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArgSerTh 344
Db 652 GGAGCAGCTTCAGCAGCAGCAGCGCGCTGGCGCGCGCGCGCGCGCGCTCCCGCGCGC 593

QY 344 rLeuHisArgPheGlyAsnThrSerSerSerIleThrPyrGluLeuAlaTyrIle 364
Db 592 GCTGCACCGCTTCGGCAACACCTCAAGCAGCAGCATCTGGTACGAGCTGGCGTACCTGGA 533

QY 364 uAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuLysSerGlyPh 384
Db 532 GCCAAGGCGCGCTCCCGCGCGCGCGCGCTCGGCGCGCTGCGCTGCGGTGGGCTT 473

QY 384 eLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThrAsnSerPr 404
Db 472 CAAGTGCAACAGCGCGGTGTGGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGC 413

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Qy 404 oTtpGluHisCysIleAspArgTyrProValLysIleAspSer 418
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Db 412 CTGGCTGGACTGCATCGACAGTACCGCGGCGCATGACGCC 370

RESULT 5
BQ510080 915 bp mRNA linear EST 22-JUL-2002
LOCUS EST617495 Generation of a set of potato cDNA clones for microarray
DEFINITION analyses mixed potato tissues Solanum tuberosum cDNA clone STMHH64
3' end, mRNA sequence.
ACCESSION BQ510080
VERSION BQ510080.2 GI:21925787
KEYWORDS EST
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 915)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Karamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
On Jun 10, 2002 this sequence version replaced gi:21368949.
Other ESTs: EST617494
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatostgr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdna@resgen.com
Seq primer: 57.

FEATURES
source Location/Qualifiers
1..915
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjete"
/db_xref="taxon:4113"
/clone="STMHH64"
/microarray analyses mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
of tubers, or roots."
BASE COUNT 234 a 158 c 238 g 285 t
ORIGIN

Alignment Scores:
Pred. No.: 3,74e-110 Length: 915
Score: 982.50 Matches: 197
Percent Similarity: 78.93% Conservative: 39
Best Local Similarity: 65.89% Mismatches: 59
Query Match: 43.67% Indels: 4
DB: 14 Gaps: 3

SEQ14-JOIN-SEQ4 (1-432) x BQ510080 (1-915)
Qy 37 SerSerArgAsnGlyThrCysAspSerSerTriPheLeuArgLysIleGln 56
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 25 TCACGGCTACCGGTGATTTTCATGAGTCGTCG---CTTGAGTTTCAGAGCAATTCG 81
Qy 57 GluArgSerGlyLeuGlyAspGluThrHisGlyProGluGlyLeuGlnValProPro 76
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 82 GAACGTTCTCGCTCGCGGACAACTATGTCCTGAGCTATGCATCAGCTTCCTCCG 141
Qy 77 ArgLysThrPheAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGlu 96
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Db 142 CAGCCTTCTATCGAGGCTCGGAGGAGAGGCTGAGCAAGTTATGTTTGGTGCACGGAC 201
Qy 97 AsnLeuPheLysAsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSer 116
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 202 AAATTTGTTTGTCTATACCTCTGTGAAACCTAGAAAATAGGTGCTTGTGTGATTTGT 261
Qy 117 SerMetPheAsnProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArg 136
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 262 AGTTTGTTCATTCACGACCTCCCTTTCAGCTATGATGTGTGAACAAGTATAAGTTGAGA 321
Qy 137 SerAsnValArgSerPheAsnLeuGlyIleMetGlyCysSerAlaGlyValIleAlaIle 156
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 322 GGTAAATATAAGCAGTTTAAATCTGGAGGTATGGTGTGTAGTGTGCTGTAATTCGCGTT 381
Qy 157 AspLeuAlaLysAspLeuHisValHisLysAsnThrTyrAlaLeuValValSerThr 176
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 382 GATCTTGCACAGACATGTTCAAGTCGACAGAAATACCTATGCTGTGTGTGTATGATCT 441
Qy 177 GluAsnIleThrTyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCys 196
||||| ||||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 442 GAGATATTACTCAGACACTGATTTTGGGAATAAGAAGTCCATGTTGATACCAATGT 501
Qy 197 LeuPheArgValGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgArg 216
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 502 TTGTTTAGAGTCGAGGTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 561
Qy 217 SerLysTyrGluLeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPhe 236
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 562 GCGAAATATAAGCTTGTTCATGCTGTAGGACACATCGTGGGCTGTAGTATAGGCATTT 621
Qy 237 ArgCysValGlnGlnGlyAspGluAsnGlyLysIleGlyValSerLeuSerLysAsp 256
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 622 CGTTGTGTTTACCAGAACAGATGATCTGGGAAACCTGGGGTTCTTCTGTCACCAAGAT 681
Qy 257 IleThrAspValAlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIle 276
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Db 682 CTCATGGCAATCGCTGGGAGCGCTTTAGACCAATATTACTACATTTGGTCTCTGTT 741
Qy 277 LeuProLeuSerGluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLys 296
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Db 742 CTACCCATCAGTACGACGCTCTCTCTTTGGTCTCTCTATATCAAGAAAATATTTAAT 801
Qy 297 AspLysIleLysHisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIle 316
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 802 AAGCATATCAAGCT---TACATTCAGATTTCAAGTTGCGCTTTGATCATTTCTGCATA 858
Qy 317 HisAlaGlyArgAla---ValIleAspValLeu-GluLysAsnLeuAlaLeu 333
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 859 CACCTCGGTGGGAGGCGCTGTTATTGACGACCTGGGAAAAGAAATTTACAGCTG 913

RESULT 6
BQ989474 765 bp mRNA linear EST 21-AUG-2002
LOCUS OGFI17M08.yg.abl OG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
DEFINITION OGFI17M08, mRNA sequence.
ACCESSION BQ989474
VERSION BQ989474.1 GI:22405009
KEYWORDS EST
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 765)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lecture and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]

```

Department of Vegetable Crops, R.W. Michelmore Lab
University of California at Davis (UCD)
Asmudson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmil.ucdavis.edu]
belongs to contig QG_CA_Contig4873, see http://cgdb.ucdavis.edu/
for details.

Plate: QGF17 row: M column: 08.

FEATURES

source
Location/Qualifiers
1..765
/organism="Lactuca sativa"
/cultivar="L. serriola"
/db_xref="taxon:4236"
/clone="QGF17M08"
/lab_host="E. coli"
/note="vector: pBRCDNA5FIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_TISSUE=flowers pre-fertilized
TAG_SEQ=GGTTGACGGG"

BASE COUNT 219 a 182 c 163 g 201 t
ORIGIN

Alignment Scores:

Pred. No.: 1.35e-104 Length: 765
Score: 936.50 Matches: 181
Percent Similarity: 82.42% Conservative: 30
Best Local Similarity: 70.70% Mismatches: 44
Query Match: 41.62% Indels: 1
DB: 14 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x B0989474 (1-765)

QY 85 GluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThrAsnVal 104
DB 1 GAGGAGCGGAGCAGGTTATGTACGAGCTTTAGATAATCTGTTTCCAGTACCGGAGTT 60
QY 105 AsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnProThrProSer 124
DB 61 AAACCAAGACATCGGCATCTGTTGTTGTAAGTGTAGCTTTGTAATCCGACTCTTCC 120
QY 125 LeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPheAsnLeu 144
DB 121 TTGCTTCCATGATCTTAACAAATACAAATTAGAGGTAACATCGGAGCTTCAATTTG 180
QY 145 GlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeuHis 164
DB 181 GCCGAATGGATGCGAGCCCGGTGTGATGCCATGCTGCCNAGGATATGTTACAG 240
QY 165 ValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsnIleTyr 184
DB 241 GTTCACCGGAATACATACACCGCTGTTGTCAGCACCGGAAACATCACCAAAATTTGTTAT 300
QY 185 AlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGlyAlaAala 204
DB 301 TTCGGGAACAAAGTCCATGCTGATCCCAATTTTATTCGATCGGTGGTTCGTCA 360
QY 205 IleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuValHisThr 224
DB 361 GTTTTACTCTCCAAACAAATCAATGATATAAGACGAGCAAAATACAAATCGTTTCATGTC 420
QY 225 ValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGlyAspAsp 244
DB 421 GTGAGAACCCCGCGGTCCATGATGAGAAAGCTTTCCGTTGCGTATATCAAGAACAGAC 480

QY 245 GluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGlyArgThr 264
DB 481 GCCGCCGAAAGAACTGGTGTCTCTTTATCAAAAGATCTCATGCAATCGCGCGCGCA 540
QY 265 ValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLysLeuLeu 284
DB 541 CTGAAGACCAACATCACTACTCTGGCCCACTTGTCTTCCAATCAGTGAACAGCTCTT 600
QY 285 PhePheValThrPheMetGlyLysLysLeuPheLysAspLysLysIleLysHisTyrTyrVal 304
DB 601 TTCCTCTGCATTTAATAATAAATAAATTTCTCAATAACAACATCAAAACC---TACATT 657
QY 305 ProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAlaValIle 324
DB 658 CTTGATTTCAAAATAGCTTTTCGACCAATTTTCGATCCACGCTGTGTGGCTGTGATT 717
QY 325 AspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
DB 718 GATGAGCTTGAGAGAAATCTGCAGCTATATACCGACACATGTTGAAGCG 765

RESULT 7

BH696317/c
LOCUS BH696317 801 bp DNA linear GSS 20-FEB-2002
DEFINITION BOMOZ47TF BO_2_3_KB Brassica oleracea genomic clone BOMOZ47, DNA sequence.

ACCESSION BH696317
VERSION BH696317.1 GI:18768933
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea.

REFERENCE 1 (bases 1 to 801)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOMOZ47TR
Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES

source
Location/Qualifiers
1..801
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMOZ47"
/note="vector: pBOM2_3_KB"
/note="vector: pBOM1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pBOM1 using BstXI linkers"

BASE COUNT 235 a 198 c 150 g 218 t

ORIGIN

Alignment Scores:
Pred. No.: 2.57e-104 Length: 801
Score: 934.50 Matches: 178
Percent Similarity: 85.66% Conservative: 31
Best Local Similarity: 72.95% Mismatches: 34
Query Match: 41.53% Indels: 2
DB: 17 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x BH696317 (1-801)

QY 174 ValSerThrGluAsnIleThrTyrAsnIleTyrAlaGlyAspAsnArgSerMetMetVal 193
DB 799 GTCAGCACCGGAGAACATCACTCAGAACTG-TACTTAGGTAAACAAACAAATCGATTGGTT 741


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Qy 350 AsnThrSerSerSerIleTrrTyrGluLeuAlaTyrIleGluAlaLysGlyArgMet 369
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Db 540 AATACTTCTCAAGTTCAATTTGGTATGAATGGCTTACATTAAGCTAAAGGAAGATG 599
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Qy 370 LysLysGlyAsnLysValTrpGlnIleAlaLeuGlySerGlyPheLysCysAsnSerAla 389
|||||
Db 600 AGAAGGGAACAGAAATTTGGCAGATTTGGAGTGGTTCAGAGTGAACAGTGT 659
|||||
Qy 390 ValTrpValAlaLeuAsnAsnValLysAlaLysThrAsnSerProTrpGluHisCysIle 409
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Db 660 GTCTGGCAGGCTATGAACATGTGAAGCTTCACCTATGAGTCCATGGAAGATGTGAT 719
|||||
Qy 410 AspArgTyrProValLys 415
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Db 720 GATAGGTATCCAGTTGAG 737

RESULT 9
BQ872186 755 bp mRNA linear EST 15-AUG-2002
LOCUS
DEFINITION
QGI13006.yg.ab1 OG_ABCDI lettuce salinas Lactuca sativa cDNA clone
BQ872186 mRNA sequence.
ACCESSION
VERSION BQ872186.1 GI:22258744
KEYWORDS
SOURCE
ORGANISM
Lactuca sativa.
Lactuca sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 755)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@veqmail.ucdavis.edu]
belongs to contig OG_CA_Contig4873, see http://cgpdb.ucdavis.edu/
for details.
Plate: QGI13 row: O column: 06.
FEATURES
source
1..755
location/Qualifiers
/organism="Lactuca sativa"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QGI13006"
/lab_host="OG_ABCDI lettuce salinas"
/lab_host="E.coli"
/Note="Vector: pBRCDNASFIAB: The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=OG_ABCDI lettuce salinas
TAG_ISSUE=roots
TAG_SEQ=GTGACGGG"
BASE COUNT 217 a 181 c 156 g 201 t
ORIGIN
Alignment Scores:

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Pred. No.: 5.19e-102 Length: 755
Score: 915.50 Matches: 176
Percent Similarity: 82.80% Conservative: 31
Best Local Similarity: 70.40% Mismatches: 42
Query Match: 40.69% Indels: 1
DB: 14 Gaps: 1

SQ14-JOIN-SEQ4 (1-432) x BQ872186 (1-755)

Qy 86 GluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsnThrAsnValAsn 105
|||||
Db 3 GAGCGGAGCAGGTTATACGAGCTTTAGATAATCTGTTTCCAGTACCGAGGATTTAA 62
|||||
Qy 106 ProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnProThrProSerLeu 125
|||||
Db 63 CCAAAAGACATCGGCATCTTGTGGTGAACGTGAGCTTGTCAATCCGACTCCTTCCTG 122
|||||
Qy 126 SerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPheAsnLeuGly 145
|||||
Db 123 TCTTCCATGATCGTTAACAAATACAAATTAAGAGGTAAACATCCGAGCTTCAATTTGGG 182
|||||
Qy 146 GlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeuHisVal 165
|||||
Db 183 GGAATGGATGACGCGCGGTGATTGCCATCGATCTGCCAAGGATATGTACAGGTT 242
|||||
Qy 166 HisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsnIleTyrAla 185
|||||
Db 243 CACCGGAATACATACGCGCTGTTGTGACGACCGAAACATCACCCANAATTGGTATTTC 302
|||||
Qy 186 GlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyGlyAlaAlaIle 205
|||||
Db 303 GGGACAAACAGTCCATCTGTCATCCCAATTTGTTATTCGAGTCGGTCTGCAGTT 362
|||||
Qy 206 LeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuValHisThrVal 225
|||||
Db 363 TTACTCTCCACAAATCAATCGATAAAGACGACGCAAAATACAACTCGTTCATGTCGTC 422
|||||
Qy 226 ArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGlyAspGlu 245
|||||
Db 423 AGAACCCACCGTGTGCAGATGAGAAAGCTTTCCGTTGCGTATATCAAGAACAGACGCC 482
|||||
Qy 246 AsnGlyLysIleGlyValSerLysAspIleThrAspValAlaGlyArgThrVal 265
|||||
Db 483 GCGGGAACAACTGGTGCTCTTTATCAAAAGATCTCATGCCAATCGCGCGGCGGACTG 542
|||||
Qy 266 LysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLysLeuLeuPhe 285
|||||
Db 543 AAACCAACATCACTACTCTGGGCCCTTGTCTTCTCAATCAACATCAACCC---TACATCT 602
|||||
Qy 286 PheValThrPheMetGlyLysLysLeuPheLysAspLysHisTyrTyrValPro 305
|||||
Db 603 TTCTGCATTTTAATAATAAATAATTTCTTAATAACAACATCAACCC---TACATCTCT 659
|||||
Qy 306 AspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAlaValIleAsp 325
|||||
Db 660 GATTTCAAAATTAAGCTTTGACACCTTTCTGCATCCACGCTGGTGGTGGCTGTGATGAT 719
|||||
Qy 326 ValLeuGluLysAsnLeuAlaLeuAlaPro 335
|||||
Db 720 GAGCTTGAGAAAGATCTGCAGCTATACCCG 749

RESULT 10
BQ855453 770 bp mRNA linear EST 14-AUG-2002
LOCUS
DEFINITION
QGI26K03.yg.ab1 OG_ABCDI lettuce salinas Lactuca sativa cDNA clone
BQ855453 mRNA sequence.
ACCESSION
VERSION BQ855453.1 GI:22240918
KEYWORDS
SOURCE
ORGANISM
Lactuca sativa.
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

```


Alignment Scores:

Pred. No.: 1,08e-98 Length: 735
 Score: 888.50 Matches: 171
 Percent Similarity: 82.86% Conservative: 32
 Best Local Similarity: 69.80% Mismatches: 41
 Query Match: 39.49% Indels: 1
 DB: 12 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x BG6599761 (1-735)

Qy 124 SerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPheAsn 143
 Db 4 TCCTTCGCGCATGATGTTAATCATATATAACATTAGGGGAATGTTATTAGCTACAT 63
 Qy 144 LeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeuLeu 163
 Db 64 CTTGGTGGAAATGGTGTAGTGGTGTGATGATGATGATGATGATGATGATGATGATGAT 123
 Qy 164 HisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsnIle 183
 Db 124 CAAGTCCATCCCAACACATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
 Qy 184 TyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyAla 203
 Db 184 TATTTGGTAAATGAGAAATCCATGCTCTCCGAATGTTATTCCGGATGGGTGGT 243
 Qy 204 AlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeuValHis 223
 Db 244 GCTGTGCTCTCAATAAACGATCTGATAGGAACGATCAACAGTACAGCTGCTGCAT 303
 Qy 224 ThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlyAsp 243
 Db 304 ACTGTAGAACACCAAAAGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 363
 Qy 244 AspGluAsnGlyLysIleGlyValSerLysLeuSerLysAspIleThrAspValAlaGlyArg 263
 Db 364 GATTCGGATGGAAAGATTGGGCTCTCTGTCAAAAGAGCTAATGGCAGTAGCTGGCGAT 423
 Qy 264 ThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSerGluLysLeu 283
 Db 424 GCTCTGAGACAAACATCACACATATTAGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
 Qy 284 LeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyrTyr 303
 Db 484 CTTTTCCTCCACATTTGGTGGGAAGGAGCTATTGAAGGCGGAAGATAGGCCT---TAT 540
 Qy 304 ValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArgAlaVal 323
 Db 541 ATCCCTGATTTTAAGTTAGCATTTTGCATTTCTGCATTCATGCTGGTGGGAAGAGCTGTA 600
 Qy 324 IleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArgSer 343
 Db 601 CTGGATCACTAGAGAAACCTCAGCTCTCTGATTTGGCATATGGAGCCTTCACGATG 660
 Qy 344 ThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTrpTyrGluLeuAlaTyrIle 363
 Db 661 ACATTCATCATGATTTGGCAACACTTCAAGCAGCTCCCTTTGGTACGAATGGCCTATTGG 720
 Qy 364 GluAlaLysGlyArg 368
 Db 721 GAAGCCAAAGGATAGG 735

RESULT 12
 BG646966
 LOCUS EST508585 HOGA Medicago truncatula cDNA clone phOGA-15E18 5' end,
 DEFINITION mRNA sequence.
 ACCESSION BG646966
 VERSION BG646966.1 GI:13782078
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.

1 (bases 1 to 800)
 Hahn.M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
 Utterback,T., Cho,J. and Fraser,C.M.
 ESTs from roots of Medicago truncatula treated with
 oligogalacturonides of DP 6-20

JOURNAL
 COMMENT
 Contact: Michael G. Hahn
 Unpublished (2001)
 Complex Carbohydrate Research Center
 University of Georgia
 220 Riverbend Road, Athens, GA 30602-4712, USA
 Tel: 706-542-4457
 Fax: 706-542-4412
 Email: hahn@ccrc.uga.edu
 G90572e TIGR sequence name: MTMBT33TK More information is
 available at: www.medicago.org
 Seq primer: SKmod (CTA gAA gTg gAT CC).
 Location/Qualifiers
 1. 800

FEATURES
source

/organism="Medicago truncatula"

/cultivar="A17"

/db_xref="taxon:3880"

/clone="phOGA-15E18"

/clone_lib="HOGA"

/tissue_type="3 day old seedling roots"

/dev_stage="24 hours after treatment in the dark at 26 C
 with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
 presence of 100 ug/ml Gentamicin"

/lab_host="XLOLR"

/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI: cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the Unizap XR vector from
 Stratagene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-zap phage using Ex-assist
 helper phage and propagated in SOLR cells."

BASE COUNT 242 a 157 c 177 g 224 t

ORIGIN

Alignment Scores:

Align. No.: 3,84e-98 Length: 800
 Score: 884.50 Matches: 171
 Percent Similarity: 81.23% Conservative: 41
 Best Local Similarity: 65.52% Mismatches: 47
 Query Match: 39.31% Indels: 2
 DB: 12 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x BG646966 (1-800)

Qy 72 LeuGlnValProProArgLysThrPhe-AlaAlaAlaArgGluGluThrGluGlnValI 91
 Db 2 ATGAGGGTCCCACTTAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 61
 Qy 91 eileGlyAlaLeuGluAsnLeuPheLysAsnThrAsnValAsnProLysAspIleGlyI 111
 Db 62 GTTGTGCTGATTTGATGAGTTCTTCAAAAACCTGCTGTGAAGGCTAAGGATATTGGGAT 121
 Qy 111 eLeuValValAsnSerSerMetPheAsnProThrProSerLeuSerAlaMetValValAs 131
 Db 122 TTTGGTGTGGAATGTAGTTGTTTAAATCCACACCATCTCTTCTGCCATGATTGTGAA 181
 Qy 131 nThrPheLysLeuArgSerAsnValArgSerPheAsnLeuGlyGlyMetGlyCysSerAl 151
 Db 182 TCATTATAAGTTGAGAGAAATATCTTGATTTAATAATCTTGTGTGATGATGATGATGATG 241
 Qy 151 aGlyValIleAlaIleAspLeuAlaLysAspLeuHisValHisLysAsnThrTyrAl 171
 Db 242 TGGTCTTATCTATTGACCTTGCCTGCAACAGCTCTCTACAGGTACATCCAACTCATATGC 301
 Qy 171 aLeuValValSerThrGluAsnIleThrTyrAsnIleThrTyrAlaGlyAspAsnArgSerMe 191

```

|||||
Db 302 CTTAGTAGGAGGAGGAGACATTAACACTGGAATTTTCGCAACACAGATCAAT 361
Qy 191 tmetValSerAsnCysLeuPheArgValGlyGlyAlaAlaIleLeuLeuSerAsnLysPr 211
Db 362 GCTAGTCCCAATGCTCTTTAGAAATGGGAGGAGCAGAGTCTCTCTCCCAACAGCC 421
Qy 211 oGlyAspArgArgSerLysTyrGluLeuValHisThrValArgThrHisThrGlyAl 231
Db 422 ACGGAGCGGCTCCGATCAAAATACCAACTAGTCCACACCGTCCGACGACCAAGGTCG 481
Qy 231 aAspGlyLysSerPheArgCysValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 251
Db 482 AGACAACAAATCTACCGCTGGCTCTTCAAGAAGAGAGACACAAAGAACGATCGGTGT 541
Qy 251 lserLeuSerLysAspIleThrAspValAlaGlyArgThrValLysLysAsnLeAla 271
Db 542 ATCACTCTCAAAAGACCTAATGGCTGTGGCGGAGAGCACTCAAAACAAACATCAAC 601
Qy 271 rLeuGlyProLeuIleLeuProLeuSerGluLysLeuLeuPhePheValThrPheMetG 291
Db 602 ATTAGGACCATTAGTCTACCTATGTGCGAACAGCTCTTATTTTCGGGACATTGGTTC 661
Qy 291 yLysLeuPheLysAspLysLysLysLysLysLysLysLysLysLysLysLysLysL 311
Db 662 CCGAAATCTTCAAGATCAAAATAAACCA---TACATTCCTGATTTTAAATTAGCTTT 718
Qy 311 eAspHisPheCysIleHisAlaGlyArgAlaValIleAspValLeuGluLysAsnLe 331
Db 719 TGAGCATTTTGTATTCATGCTGTGGTGGAGAGCGCTGTTGGATGAGTGGAGAAATCT 778
Qy 331 u 331
Db 779 G 779

RESULT 13
LOCUS BE055710
DEFINITION GA_Ea0035J01f Gossypium arboreum 7-10 dpa fiber library Gossypium
ACCESSION BE055710
VERSION BE055710.2
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.
REFERENCE 1 (bases 1 to 840)
AUTHORS Wing R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Leslie, A. and Wilkins, T.A.
TITLE An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT On Jun 8, 2000 this sequence version replaced gi:8382767.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCATATAGGG
High quality sequence stop: 659.
FEATURES
Location/Qualifiers
1..840
/organism="Gossypium arboreum"
/strain="AXA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0035J01f"
/tissue_type="Fibers isolated from bolls harvested 7-10

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dpaa"
/lab_host="E. coli"
/note="vector: pbk-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 238 a 173 c 198 g 229 t 2 others
ORIGIN
Alignment Scores:
Pred. No.: 3,04e-97 Length: 840
Score: 877.50 Matches: 187
Percent Similarity: 78.87% Conservative: 37
Best Local Similarity: 65.85% Mismatches: 56
Query Match: 39.00% Indels: 7
Db: 10 Gaps: 2
SEQ14-JOIN-SEQ4 (1-432) x BE055710 (1-840)
Qy 104 ValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnProThrPro 123
Db 1 GTAAACCCCAAGACATTTGGAATTTTGGTGTGCACTGCACTGCGAGCTTGTAAATCCACGCCA 60
Qy 124 SerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSerPheAsn 143
Db 61 TCTTTGCTGCCATGGTTATCAACCATTAAGCTTCGAGGGAATATTCAAAGCTACAC 120
Qy 144 LeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAspLeuLeu 163
Db 121 TTGGAGGAATGGGCTGTAGTGGTGTCTCTCAATAGATCTTGCAGGAATCTACTTT 180
Qy 164 HisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyrAsnIle 183
Db 181 CAAGTCCATCCGAACCTCTATGCACTGGTTATCAGCATGGAGAACATCACCTTGAACCTG 240
Qy 184 TyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGlyAla 203
Db 241 TACTTTGGAAATGTCGCTCAAAACTTGTTCAAACTGCTTATTCAGATGGGAGGCGCG 300
Qy 204 AlaIleLeuLeuSerAsnLysProGlyAspArgArgArgSerLysTyrGluLeuValHis 223
Db 301 GCAATACTGCTCTCTAACAAACGCTCTGACAGAAGAGATCCAAATACCAATGGTTCAC 360
Qy 224 ThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGlnGlnG 243
Db 361 ACTGTCGCACTCACAAAGGCGCGGAGTAAAGTGTGCTTGTGTTACACAGAGAA 420
Qy 244 AspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAlaGlyArg 263
Db 421 GACTCTCGAGAAGATGGCTTACATGTTCAGAGATCTCATGCGAGTTCCTGGTGAT 480
Qy 264 ThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGluLysLeu 283
Db 481 GCTCTAAGACCAACATCAACATTTGGGCGCTCTGTTCTTCCGATGCTGAGCAGCTG 540
Qy 284 LeuPhePheValThr-PheMetGlyLysLysLeuPheLysAspLysIleLysHisTyrTy 303
Db 541 CTNTCTTCTCTACATTTGGTGGGAAAGACCTATCANAAATGAAGATCAAGCT---TA 597
Qy 303 rVal-ProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArgAlav 323
Db 598 CATTTCCAGATTTCAAGTAGCTTTTGAACATTTCTGCAATTCACGCTGGAGGAAGACTG 657
Qy 323 alIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSerArg 343
Db 658 TTTTGTGTAACCTGGAGAAGATTTTGCAGCTCTCCGAATGGCATATGGACCATTCANAA 717
Qy 343 erThrLeuHisArgPheGlyAsnThrSerSerSerIleTrpTyrGluLeuAlaTyrI 363
Db 718 TGACTCTCTT-CGAATTTGGAAA---CCTCAAGCAGCTCTCTGGGTATGATGGCTATC 773
Qy 363 leGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGlySerg 383
Db 774 CGGAGGCTTAGGGAGGATTAGGAAGGAACCAACACC-TGGCAAAA-GCATTTGGTCTCTG 831
Qy 383 lyPheLys 385

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|||||||
Db 832 GATTCAA 839

RESULT 14
BH512254 769 bp DNA linear GSS 13-DEC-2001
LOCUS BOHKU08TF BOHK Brassica oleracea genomic clone BOHKU08, DNA
DEFINITION
ACCESION BH512254
VERSION BH512254.1 GI:17720344
KEYWORDS GSS
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL 1 (bases 1 to 769)
COMMENT Whole genome shotgun sequencing of Brassica oleracea
Other_GSSs: BOHKU08TR
Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..769
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHKU08"
/clone_lib="BOHK"
/note="Vector: pHOS1; site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT 195 a 204 c 159 g 211 t
ORIGIN

Alignment Scores:
Pred. No.: 1,1e-96 Length: 769
Score: 872.50 Matches: 170
Percent Similarity: 96.65% Conservative: 3
Best Local Similarity: 94.97% Mismatches: 5
Query Match: 38.78% Indels: 1
Dbs: 17 Gaps: 1

SEQ14-JOIN-SEQ4 (1-432) x BH512254 (1-769)
QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisLeuArgValSerVal 21
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Db 236 CGGTTTACCTCGTGGTACTCATGCTACCTCCACCAACGATTTGTAGATCAAGTATC 295
QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41
|||||||
Db 296 TCCAAAGGTTCATGATATCTTTTACCAGTACAGAAACCTGAT---CCTTCTCGGAACGCG 352
QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
|||||||
Db 353 ACCTGCGATGACTCGCTCGTGGTCTGACTTCTTGAGGAAGATTCAAGAAGCTTCAGGCTCA 412
QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
|||||||
Db 413 GCGGATGAAACCCACGCGCGCGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTCG 472
QY 82 AlaAlaArgGluGluThrGluGlnValIlelleGlyAlaLeuGluAsnLeuPheLysAsn 101
|||||||
Db 473 GCGGCGCGTGAAGACGAGCAGGTATTCATTCGTGCGGTAGAAATCTATTCAAGAAC 532
QY 102 ThrAsnValAsnProLysAspIlelleGlyLeuValValAsnSerSerMetPheAsnPro 121
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Db 533 ACCAATGTTAACCCCTACAGATATAGTATAGTGTGGTGAAGTCAAGCATGTTTAAATCCA 592
QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuValArgSerValArgSer 141
|||||||
Db 593 ACTCCTTCGCTCTCCGCGATGCTGCTTAACACTTTCAGCTCCGAAGCAACGTAAAGAC 652
QY 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
|||||||
Db 653 TTTAACTTGTGGTCATGGTGTAGTCCCGCGCTTATAGCCATTCATCTAGCAAGGAC 712
QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
|||||||
Db 713 TTGTTGATGTCATAATAATACGTATGCTCTGTGTGTGAGCAGACAGAGAATCATCACT 769
RESULT 15
BH512254
LOCUS HVSMEI0014L13f Hordeum vulgare spike EST library HVCDNA0012
DEFINITION (Fusarium infected) Hordeum vulgare cDNA clone HVSMEI0014L13f, mRNA
sequence.
ACCESION BH512254
VERSION BH512254.1 GI:16290960
KEYWORDS EST
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
1 (bases 1 to 867)
; Triticeae; Hordeum.
Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhofs,A., Wise,R., Heinen
,S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
Simmons,J., Fenton,R.D., Malatrasi,M., Choi,D.W., Oates,R. and Main
D.
Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases: 355
Seq primer: AATTAAACCTCTCACTAAAGG
High quality sequence stop: 610.
Location/Qualifiers
1..867
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEI0014L13f"
/clone_lib="Hordeum vulgare spike EST library HVCDNA0012"
(tissue_type="Spike")
/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; plants were grown at the University of Minnesota in
the GJ Muehlbauer lab; spikes were harvested and snap
frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
graminearum inoculation (Heinen). In the TJ Close lab at
the University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all
eight RNA pools were combined, poly(A) RNA was purified
from the mixture, one primary unamplified cDNA library was
made, and 1 million pfu were in vivo excised to give
pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi
). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch Atkins and Wing) plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
```

The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley/>. To order this clone see <http://www.genome.clemson.edu/orders/Also> see Close TJ, Wang R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. *Barley Genetics Newsletter* 31:29-39. (<http://wheat.pw.usda.gov/ggpages/gdn/31/cover.html>).

BASE COUNT	200 a	223 c	260 g	182 t	2 others
ORIGIN					

Alignment Scores:	1.76e-96	Length:	867
Pred. No.:	871.50	Matches:	188
Score:	80.3%	Conservative:	33
Percent Similarity:	80.3%	Mismatches:	53
Best Local Similarity:	68.3%	Indels:	6
Query Match:	38.73%	Gaps:	1
DB:	13		

SEQ14-JOIN-SEQ4 (1-432) x BI949576 (1-867)

Qy	119	PheAsnProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsn	138
Db	2	TTCAACCCGACCGCTCACTCGCCATCGTGGTGAACCATTTACAAGCTGAGAGGAAC	61
Qy	139	ValArgSerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeu	158
Db	62	ATAATCAGCTACAATCTGGGGAATGGGTCAGTCGCGGCTCTGTCCATAGATCTG	121
Qy	159	AlaLysAspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsn	178
Db	122	GCCAAGGATTGCTTCAGGTGCATCCCACTCGTACGCCATGTGTGAGCACCAGGAAC	181
Qy	179	IleThrTyrAsnIleTyrAlaGlyAspAsnArgSerMetValSerAsnCysLeuPhe	198
Db	182	ATTACCCTGAATTGTTATTTGGGAACAACCGCTCGATGCTGTCGTCAATTGCTCTTC	241
Qy	199	ArgValGlyValAlaIleLeuLeuSerAsnLysProGlyAspArgArgCysSerLys	218
Db	242	CGATGGGTTCGCTCGCATCTCTGTCGAACAGCGTCACAGAGAGGTCCAG	301
Qy	219	TyrGluLeuValHisThrValIArgThrHisThrGlyAlaAspGlyLysPheArgCys	238
Db	302	TACGAGCTGGTACACCGCTGAGAACTACAAGGTGCAGATGCAAGTGTCTCAGCTGT	361
Qy	239	ValGlnGlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThr	258
Db	362	GTCAACCGAGGAGGATGACAGTGGCAGGTTGGCTGCCACTGTCTCCAAAGACCTCATG	421
Qy	259	AspValAlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuPro	278
Db	422	CGGTGTGCTGGGATCGCCTCAGACGAACATCAACAGCTTGGCGGTGTGTGTGCCA	481
Qy	279	LeuSerGluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLys	298
Db	482	TTCTCGGAGCAGCTGCTTTCATGGTCACATGGTTGGCAAGAAGCTGTTCAGATGAAG	541
Qy	299	IleLysHisTyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAla	318
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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 6, 2003, 14:56:55 ; Search time 187 seconds
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Searched: 2185239 seqs, 1125999159 residues

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2238	99.2	1521	24	AAD28510	A. thaliana FAEL-B
5	2236	99.2	1521	24	AAD28503	A. thaliana FAEL-B
6	2235	99.1	1521	24	AAD28507	A. thaliana FAEL-B
7	2232	99.0	1521	24	AAD28535	Alternative versio
8	2208.5	97.9	1518	24	AAD28504	A. thaliana FAEL-B
9	2208.5	97.9	1518	24	AAD28501	Brassica napus fat
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13	2201.5	97.6	1785	22	AAF61744	B. napus KCS cDNA
14	2201.5	97.6	1785	22	AAF61746	B. napus KCS cDNA
15	2201.5	97.6	1790	22	AAF62741	Brassica napus FAE
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17	2177	96.5	1521	24	AAD28536	Alternative versio
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19	2156.5	95.6	1521	24	AAD28515	Brassica napus elo
20	2156	95.6	1521	24	AAD28511	A. thaliana FAEL-B
21	2155	95.6	1521	24	AAD28518	A. thaliana FAEL-B
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23	2149.5	95.3	1521	24	AAD28520	B. napus elongase
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32	1857.5	82.4	1664	16	AAQ90211	Brassica condensin
33	1649	73.1	4313	24	AAI27086	Condensing enzyme
34	1519.5	67.4	1611	20	AAI23221	DNA sequence of Lf
35	1519.5	67.4	1853	21	AAC50224	A. thaliana EL5 DN
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37	1503.5	66.7	1548	20	AAX23223	A. thaliana EL7 DN
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ALIGNMENTS

RESULT 1
AAD28505
ID AAD28505 standard; DNA; 1521 BP.

AC AAD28505;

DT 22-APR-2002 (first entry)

DE A. thaliana FAEL-B. napus elongase KCS chimeric gene, At114 mutant #1.

KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;

KW very long chain fatty acid; VLCFA; FAEL gene; chimeric; mutant; ds.

XX Chimeric - Arabidopsis thaliana.

OS Chimeric - Brassica napus.

XX Key Location/Qualifiers

FT CDS 1..1521

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XX      13-DEC-2001.
XX      08-JUN-2001; 2001WO-US18737.
XX      08-JUN-2000; 2000US-210326P.
XX      (UYMI-) UNIV MIAMI.
XX      Jaworski JG, Blacklock BJ;
XX      WPI: 2002-154572/20.
XX      P-PSDB; AAE17613.
XX      New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
XX      acids encoding the polypeptide, useful for producing very long chain
XX      fatty acids -
XX      Disclosure; Fig 2-6; 139pp; English.
XX      The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
XX      (KCS) polypeptides with altered substrate specificity and/or catalytic
XX      activity and nucleic acid molecules encoding such polypeptides.
XX      Polypeptides of the invention are useful for catalysing the condensation
XX      of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
XX      of C20 fatty acyl CoA. They are especially useful for producing very
XX      long chain fatty acids (VLCFA) and may be used in the development of
XX      reagents for various purposes, e.g., immunological reagents to monitor
XX      expression of elongase KCS polypeptides or nucleic acid probes or
XX      primers to monitor inheritance of an elongase KCS gene in plant breeding
XX      programs. The present sequence is a mutant of Arabidopsis thaliana FAEL-
XX      Brassica napus elongase KCS chimeric gene, At114 designated as
XX      At114 L91C K92R.
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XX DT 22-APR-2002 (first entry)
XX DE A. thaliana FAEL-B. napus elongase KCS chimeric gene, At114 mutant #4.
XX KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
XX KW very long chain fatty acid; VLCFA; FAEL gene; chimeric; mutant; ds.
XX OS Chimeric - Arabidopsis thaliana.
XX OS Chimeric - Brassica napus.
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XX 08-JUN-2001; 2001WO-US18737.
XX 08-JUN-2000; 2000US-210326P.
XX (UYMI-) UNIV MIAMI.
XX Jaworski JG, Blacklock BJ;
XX WPI: 2002-154572/20.
XX P-PSDB; AAE17617.
XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
XX acids encoding the polypeptide, useful for producing very long chain
XX fatty acids -
XX Disclosure; Fig 2-10; 139pp; English.
XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
XX (KCS) polypeptides with altered substrate specificity and/or catalytic
XX activity and nucleic acid molecules encoding such polypeptides.
XX Polypeptides of the invention are useful for catalysing the condensation
XX of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
XX of C20 fatty acyl CoA. They are especially useful for producing very
XX long chain fatty acids (VLCFA) and may be used in the development of
XX reagents for various purposes, e.g., immunological reagents to monitor
XX expression of elongase KCS polypeptides or nucleic acid probes or
XX primers to monitor inheritance of an elongase KCS gene in plant breeding
XX programs. The present sequence is a mutant of Arabidopsis thaliana FAEL-
XX Brassica napus elongase KCS chimeric gene, At114 designated as
XX At114 L91C K92R G307D.
XX Sequence 1521 BP; 415 A; 340 C; 423 T; 0 other;

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AC AAD28506;
XX
DT 22-APR-2002 (first entry)
XX
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XX
KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
RW very long chain fatty acid; VLCFA; FAEL gene; chimeric; mutant; ds.
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OS Chimeric - Arabidopsis thaliana.
OS Chimeric - Brassica napus.
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XX
XX (UYMI-) UNIV MIAMI.
XX
XX Jaworski JG, Blacklock BJ;
XX
XX WPI; 2002-154572/20.
XX
XX P-PSDB; AAE17614.
XX
XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
XX acids encoding the polypeptide, useful for producing very long chain
PT
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PT fatty acids -
XX
PS Disclosure: Fig 2-7; 139pp; English.
XX
CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
CC (KCS) polypeptides with altered substrate specificity and/or catalytic
CC activity and nucleic acid molecules encoding such polypeptides.
CC Polypeptides of the invention are useful for catalyzing the condensation
CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
CC of C20 fatty acyl CoA. They are especially useful for producing very
CC long chain fatty acids (VLCFA) and may be used in the development of
CC reagents for various purposes, e.g., immunological reagents to monitor
CC expression of elongase KCS polypeptides or nucleic acid probes or
CC primers to monitor inheritance of an elongase KCS gene in plant breeding
CC programs. The present sequence is a mutant of Arabidopsis thaliana FAEL-
CC Brassica napus elongase KCS chimeric gene, At114 designated as
XX At114 K92R.
SQ Sequence 1521 BP; 412 A; 342 C; 344 G; 423 T; 0 other;
Alignment Scores:
Pred. No.: 4,88e-235 Length: 1521
Score: 2239.00 Matches: 430
Percent Similarity: 99.54% Conservative: 0
Best Local Similarity: 99.54% Mismatches: 2
Query Match: 99.29% Indels: 0
DB: 24 Gaps: 0
SEQ12-JOIN-SEQ4 (1-432) x AAD28506 (1-1521)
Qy 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProProHisCysArgValSer 20
Db 223 AATCCGGTTTATCTGTTGACTACTCGTGTACTTCCGGCCACCGCATCTCAGAGTTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db 283 GTCTCTAAAGTCATGGATATTTTCTACCAATPAAGAAAGCTGATACTTCTTTCACGGGAC 342
Qy 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
Db 343 GGCACGTGTGATGATTCTGCTGCTTACTTCTTGAGGAAGATTCAAGAAGCTTCAGGT 402
Qy 61 LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe 80
Db 403 CTAGGCGATGAACATCAGCGGCCGAGGGGCTCTTCAGGTCTCTCCCGAAGACTTTT 462
Qy 81 AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 GCGGCGCGCGTGAAGAGACGAGCAAGTTATCATTTGGTGGCTAGAAAATCTATTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAACGTTAACCCTAAAGATATAGTATACTTGTGGTGAACCAAGCATGTTTAA 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CCAACTCCATCGCTCTCCGGATGGTCTTAACACTTTCAAGTCCCAAGCAACGTAAGA 642
Qy 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACTTGGTGGCATGGGTTGTAGTCCGCGCTTATAGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTTCATGTCATTAATAAATACGTATGCTTGTGGTGACACAGAACATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGGTGTGATATAGTCTCATGATGGTTTCAAAATTCCTTGTTCGCTGT 822
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGCGCGTATTTTGTCTCTCCAACAGCGCTGGAGATCGTAGACGGTCCAAGTACGAG 882
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Db 583 CCAACCTCCATCGCTCCCGCATGGTCTGTAAACACTTTTCAGCTCCGAAGCAAGCTAAGA 642
Qy 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys 160
Db 643 AGCTTTAACCTTGGTGGCATGGTGTAGTCCGGCGGCTTATAGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrThrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTGATGTCCATAAANAATACGATGCTCTTGTGGTGAGCAGACAGACATCAGC 762
Qy 181 TyrAsnIleThrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGGTGATAATAGGTCCATGATGTTTCAAAATGCTTTCCTCGTGT 822
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGGCCCTATTTTCTCTCCACACAGCCTGGAGATCGTAGACGTCCTCAAGTAGCAG 882
Qy 221 LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTTCACACGCTTCGAACGCATACCGGAGCTGACGACAAAGTCTTTTCGTGGTGCA 942
Qy 241 GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
Db 943 CAAGGACGATGAGAACGCAAAATCGGAGTGGATTTCTCCAAAGSACATAACCGATGTT 1002
Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
Db 1003 GCTGGTGAACGGTTAAGAAACATAGCAACGTTGGGTCGGTGTATCTTCCTCGTTAAGC 1062
Qy 281 GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys 300
Db 1063 GAGAAACTCTTTTTCGTTACCTTCATGGCAAGAAACTTTTCAAAAGATAAAATCAAA 1122
Qy 301 HisTyrThrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyCly 320
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Qy 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrThrGluLeu 360
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Qy 401 ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAAAATAGTCTTTGGGAACACATGCTACGACAGATACCGGTCAAAATGATTCTGATTCA 1482
Qy 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAAGTCAGAGACTCGTGTCCAAAACGCTCGGTCC 1518

RESULT 5
AAD28503
ID AAD28503 standard; DNA; 1521 BP.
XX
AC AAD28503;
XX
DT 22-APR-2002 (first entry)
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XX
DE A. thaliana FAEL1-Brassica napus elongase KCS chimeric gene, At114.
KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW very long chain fatty acid; VLCFA; FAEL1 gene; chimeric; ds.
XX
OS Chimeric - Arabidopsis thaliana.
OS Chimeric - Brassica napus.
XX
FH Key Location/Qualifiers
CDS 1..1521
FT /tag= a
FT /product= "A. thaliana FAEL1-Brassica napus elongase KCS
FT chimeric protein, At114"
FT
FT misc_feature 1..342
FT /tag= b
FT /note= "Arabidopsis thaliana FAEL1 gene"
FT 343..1521
FT /tag= c
FT /note= "Brassica napus elongase KCS gene"
XX
PN WO200194565-A2.
XX
XX 13-DEC-2001.
XX
XX 08-JUN-2001; 2001WO-US18737.
XX
XX 08-JUN-2000; 2000US-210326P.
XX
XX (UYMI-) UNIV MIAMI.
XX
XX Jaworski JG, Blacklock BJ;
XX
XX WPI; 2002-154572/20.
XX
XX P-PSDB; AAEL17611.
XX
XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
XX acids encoding the polypeptide, useful for producing very long chain
XX fatty acids -
XX
XX Disclosure; Fig 2-4; 139pp; English.
XX
XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
XX (KCS) polypeptides with altered substrate specificity and/or catalytic
XX activity and nucleic acid molecules encoding such polypeptides.
XX
XX Polypeptides of the invention are useful for catalysing the condensation
XX of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
XX of C20 fatty acyl CoA. They are especially useful for producing very
XX long chain fatty acids (VLCFA) and may be used in the development of
XX reagents for various purposes, e.g., immunological reagents to monitor
XX expression of elongase KCS polypeptides or nucleic acid probes or
XX primers to monitor inheritance of an elongase KCS gene in plant breeding
XX programs. The present sequence is Arabidopsis thaliana FAEL1-
XX Brassica napus elongase KCS chimeric gene designated as At114.
XX
XX Sequence 1521 BP; 413 A; 342 C; 343 G; 423 T; 0 other;
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Alignment Scores:
Pred. No.: 1,04e-234 Length: 1521
Score: 2236.00 Matches: 429
Percent Similarity: 99.54% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.16% Indels: 0
DB: 24 Gaps: 0
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SEQ12-JOIN-SEQ4 (1-432) x AAD28503 (1-1521)

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Qy 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSer 20
Db 223 AATCCGGTTTATCTGTTGACTACTCGTGTACTCTCCGCCACCGCATCTCAAAAGTTAGT 282
Qy 21 ValSerLysValMetAspPheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
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Db	283	GTCTCTAAAGTCATGATATTTTCTACCAAAATAGAAAAAGCTCATACTTCTTCAACGGAAC	342
QY	41	GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly	60
Db	343	GGCAGGTGTGATGATTCGTCTGGCTTGACTTCTTGAGGAAGATTCAAGAACGTTCCAGGT	402
QY	61	LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe	80
Db	403	CTAGGCGATGAACACTCACGGGCCCGAGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTT	462
QY	81	AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys	100
Db	463	CGCGCGCGCGGTGAAGACGCGCAAGATTATCTTTGGTGCGCTAGAAAATCTATTCAAG	522
QY	101	AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn	120
Db	523	AACACCAACGTTAACCTTAAGATATAGGTATACTTGTGGTGAAGTCAAGCATGTTTAAT	582
QY	121	ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg	140
Db	583	CCAACTCCATCGCTCTCCGCGATGCTGTTAACTTTCAAGCTCCGAAGCAAGTAAGA	642
QY	141	SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys	160
Db	643	AGCTTTAACTTGTGGCATGGGTGTAGTCCGCGGTATAGCCATTGATCTAGCAAG	702
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Db	703	GACTTGTGTGATCTCCATAAAATACGTATGCTCTTGTGGTGAGCAGACATCACT	762
QY	181	TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal	200
Db	763	TATAACATTTACCTGGTGATATAAGTCCATGATGTTTCAAAATGCTTGTCCGTGT	822
QY	201	GlyGlyAlaAlaIleLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu	220
Db	823	GGTGGGGCCGCTATTTGCTCTCCAAACGCTGGAGATCGTAGACGTCCAAGTAGAG	882
QY	221	LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln	240
Db	883	CTAGTTCCACACGGTTTCCGACGATACCGGAGCTGACGGCAAGTCTTTTCGTTGCGTCA	942
QY	241	GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal	260
Db	943	CAAGGAGCAGTGGAGAACCGGCAAAATCGAGTGAGTTTGTCCAGGACATTAACCGATGT	1002
QY	261	AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer	280
Db	1003	GCTGGTCCGACGGTTTAAAGAAAAACATAGCAACGTTGGGTCCGTTGATTTCTCCGTTAAGC	1062
QY	281	GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys	300
Db	1063	GAGAAACTTCTTTTTCGTTACCTTCATGCGCAAGAACTTTTCAAAGATANAATCAA	1122
QY	301	HisTyrTrpValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly	320
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QY	321	ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla	340
Db	1183	AGAGCCGTGATTGCTGTAGAGAAGAACCTAGCCCTAGCACCGATCGATGAGAGCA	1242
QY	341	SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTrpGluLeu	360
Db	1243	TCAGATCANAGTTACATAGATTTCGAACACTTCATCTAGCTCAATATGTTAGCTTG	1302
QY	361	AlaTyrIleGluAlaLysGlyArgMetLysGlyAsnLysValTrpGlnIleAlaLeu	380
Db	1303	GCATACATAGAACCAAGGAAGGATGAAGAAAGGTAATAAAAGTTTGGCAGATTGCTTTA	1362
QY	381	GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer	400
Db	1363	GGGTGAGGCTTTAAGTGTAAACAGTCCAGTTTGGTGGCTCTAAACAAATGTCAAAGCTTCG	1422
QY	401	ThrAsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSer	420
Db	1423	ACAAATAGTCCCTGGGAACACTGCATCGACAGATACCCGGTCAAAATGTGATTCTGATTCA	1482
QY	421	GlyLysSerGluThrArgValGlnAsnGlyArgSer	432
Db	1483	GCTAAGTTCAGAGACTCGTGTCCCAACGCGTCGGTCC	1518
RESULT 6			
AD28507	AAD28507 standard; DNA; 1521 BP.		
XX	AAD28507;		
XX	22-APR-2002 (first entry)		
DE	A. thaliana FAE1-B. napus elongase KCS chimeric gene, At114 mutant #3.		
KW	Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;		
XX	very long chain fatty acid; VLCFA; FAE1 gene; chimeric; mutant; ds.		
OS	Chimeric - Arabidopsis thaliana.		
OS	Chimeric - Brassica napus.		
XX	Key Location/Qualifiers		
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XX	WO200194565-A2.		
PN	13-DEC-2001.		
XX	08-JUN-2001; 2001WO-US18737.		
PF	08-JUN-2000; 2000US-210326P.		
XX	(UYMI-) UNIV MIAMI.		
XX	Jaworski JG, Blacklock BJ;		
PI	WPI; 2002-154572/20.		
DR	P-PSDB; AAE17615.		
XX	New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic		
PT	acids encoding the polypeptide, useful for producing very long chain		
PT	fatty acids		
XX	Disclosure; Fig 2-8; 139pp; English.		
XX	The invention relates to fatty acid elongase 3-ketoacyl CoA synthase		
CC	(KCS) polypeptides with altered substrate specificity and/or catalytic		
CC	activity and nucleic acid molecules encoding such polypeptides.		
CC	Polypeptides of the invention are useful for catalysing the condensation		
CC	of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis		
CC	of C20 fatty acyl CoA. They are especially useful for producing very		
CC	long chain fatty acids (VLCFA) and may be used in the development of		
CC	reagents for various purposes, e.g., immunological reagents to monitor		
CC	expression of elongase KCS polypeptides or nucleic acid probes or		
CC	primers to monitor inheritance of an elongase KCS gene in plant breeding		
CC	programs. The present sequence is a mutant of Arabidopsis thaliana FAE1-		
CC	Brassica napus elongase KCS chimeric gene, At114 designated as		
CC	At114 G307D.		

xx
SQ Sequence 1521 BP; 415 A; 341 C; 342 G; 423 T; 0 other;

Alignment Scores:
Pred. No.: 1,34e-234 Length: 1521
Score: 2235.00 Matches: 429
Percent Similarity: 99.94% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 99.11% Indels: 0
DB: 24 Gaps: 0

SEQ12-JOIN-SEQ4 (1-432) x AAD28507 (1-1521)

Qy 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSer 20
Db 223 AATCCGGTTATCTCGTTGACTACTCGTGTATCTTCCCGCACCCGATCTCAAGTTAGT 282
Qy 21 ValSerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsn 40
Db 283 GTCTCTAAAGTCATGATATTTCTACCAATAAGAAAAGCTGATACTTCTTCACGGAAC 342
Qy 41 GlyThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGly 60
Db 343 GGCACGTGTGATGATTCGTGCGTGGCTTGACTTCTTGAGGAAGATTCAGAACGTTACAGT 402
Qy 61 LeuGlyAspGlnThrHisGlyProGluGlyLeuLeuGlnValProArgLysThrPhe 80
Db 403 CTAGGCGGATGAACACTCACGGGCCGAGGGGTGCTTCAGGTCCCTCCCGGAAGACTTTT 462
Qy 81 AlaAlaAlaArgGluGlnThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys 100
Db 463 CCGCGCGCGCTGAGAGACGGGCAAGTATCATTTGGTGGCTAGAAAATCTATTCAAG 522
Qy 101 AsnThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsn 120
Db 523 AACACCAACGTTAACCTTAAGATATAGGTATATCTTGTGGTGAACCTCAAGCATGTTAAT 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
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Db 643 AGCTTTAACCTTGGTGGCATGGTGTAGTCCGCGCTTATGCCATTGATCTAGCAAG 702
Qy 161 AspLeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThr 180
Db 703 GACTTGTGTCATGCCATAAAATACGTATGCTCTTGTGTCGAGCACAGAGAATCACT 762
Qy 181 TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal 200
Db 763 TATAACATTTACGCTGGTGATATAGGTCCATGATGTTTCAANTTCTTGTTCCTGTT 822
Qy 201 GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGlu 220
Db 823 GGTGGGCGCGTATTTTGTCTCCCAACAGCTGGAGATCGTAGACGGTCCAAGTACAG 882
Qy 221 LeuValHisThrValValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 240
Db 883 CTAGTTCACAGGTTTCAACGGATACCGGAGCTGACCAAGTCTTTTCTGTTGCGTGCAA 942
Qy 241 GlnGlyAspAspGluAsnGlnLysIleGlyValSerLeuSerLysAspIleThrAspVal 260
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Qy 261 AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSer 280
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Qy 301 HisTyrTyrValProaspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly 320
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Qy 321 ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla 340
Db 1183 AGAGCGGTGATTGATGTCTAGAGAAGAACCTAGCCCTAGCACCAGTCGATGTAGAGCA 1242
Qy 341 SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrPtyrGluLeu 360
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Qy 361 AlaTyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeu 380
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Qy 381 GlySerGlyPheLysCysAsnSerAlaValTyrValAlaLeuAsnValLysAlaSer 400
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Qy 401 ThrAsnSerProTyrGluHisCysIleAspArgTyrProValLysIleAspSerAspSer 420
Db 1423 ACAATATAGTCTTGGGAACACTGCATCGACAGATACCGGTCMAAATTTGATTCTGATTCA 1482
Qy 421 GlyLysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1483 GGTAAAGTCAGAGACTCGTGTCACAAAGCGTCGTC 1518
RESULT 7
AAD28535
ID AAD28535 standard; DNA; 1521 BP.
AC AAD28535;
XX 22-APR-2002 (first entry)
DT Alternative version of At114 gene.
DE Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW very long chain fatty acid; VLCFA; FAEL gene; chimeric; ds.
XX Chimeric - Arabidopsis thaliana.
OS Chimeric - Brassica napus.
XX Key Location/Qualifiers
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FT chimeric protein, At114"
FT /transl_except= (pos:1315..1317, aa:Xaa)
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FT misc_feature 343..1521
FT /*tag= c
FT /note= "Brassica napus elongase KCS gene"
XX WO200194565-A2.
PN 13-DEC-2001.
XX 08-JUN-2001; 2001WO-US18737.
XX 08-JUN-2000; 2000US-210326P.
XX (UWMI-) UNIV MIAMI.
XX Jaworski JG, Blacklock BJ;
XX WPI: 2002-154572/20.
DR P-PSDB; AAEL7848.
XX

PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids

PS Disclosure: Page 71-74; 139pp; English.

XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
 CC of C20 fatty acyl CoA. They are especially useful for producing very
 CC long chain fatty acids (VLCFA) and may be used in the development of
 CC reagents for various purposes, e.g., immunological reagents to monitor
 CC expression of elongase KCS polypeptides or nucleic acid probes or
 CC primers to monitor inheritance of an elongase KCS gene in plant breeding
 CC programs. The present sequence is an alternative version of
 CC Arabidopsis thaliana FAEL-Brassica napus elongase KCS chimeric gene
 CC designated as At114.

XX Sequence 1521 BP; 413 A; 342 C; 342 G; 423 T; 1 other;

Alignment Scores:

Pred. No.:	2,85e-234	Length:	1521
Score:	2322.00	Matches:	428
Percent Similarity:	99.31%	Conservative:	1
Best Local Similarity:	99.07%	Mismatches:	3
Query Match:	98.98%	Indels:	0
DB:	24	Gaps:	0

SEQ12-JOIN-SEQ4 (1-432) x AAD28535 (1-1521)

QY	1	AsnProValThrLeuValAspThrSerCysThrLeuProProHisCysArgValSer	20
DB	223	ATACGGGTATCTCGTGTGACTACGCTGTGTACCTCCGCCCGCATCTCAAGGTAGT	282
QY	21	ValSerLysValMetAspIlePheThrGlnIleArgLysAlaAspThrSerSerArgAsn	40
DB	283	GTCTCTAAAGTCATGGATATTTTACCAAAATAAGAAAGCTGATCTCTTTCACGGAAAC	342
QY	41	GlyThrCysAspAspSerSerThrLeuAspPheLeuArgLysIleGlnIleArgSerGly	60
DB	343	GGCAGCTGTGATGATTCGTGGCTGACCTCTTGAGGAAGATTCAAGACGTTCAAGT	402
QY	61	LeuGlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPhe	80
DB	403	CTAGCGGATGAACCTCACGGGGCCCGAGGGGCTCTTCAGGTCCCTCCCGGAAGACTTTT	462
QY	81	AlaAlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLys	100
DB	463	GGGGGGCGCGTGAAGAGACGGCAAGTTATCATTTGTCGCTAGAAAAATCTATTCAAG	522
QY	101	AsnThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsn	120
DB	523	ACACCAACCGTTAACCCCTAAGATATAGGTATCTTGTGGTGAACCAAGCATGTTAAT	582
QY	121	ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg	140
DB	583	CCAACTCCATCGCTCCCGGATGTCGTTAACACTTTCAAGCTCCGAGCAACGTAAGA	642
QY	141	SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLys	160
DB	643	AGCTTTAACTTGTGTGATGGGTTGATGTCGGCGCTTATAGCCATTGATCTAGCAAG	702
QY	161	AspLeuLeuHisValHisLysAsnThrThrAlaLeuValValSerThrGluAsnIleThr	180
DB	703	GACTTGTGTGATGTCCTCAATAAATACGTATGCTCTGTGGTGACACAGAACATCACT	762
QY	181	TyrAsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgVal	200
DB	763	TATAACATTTCGCTGCTGATATAGTCCATGATGTTGTTCAAAATGCTGTTCGCGTGT	822
QY	201	GlyGlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysThrGlu	220

DB	823	GGTGGGGCCGCTATTTGCTCCCAACAGCTGGAGATCGTAGACGGTCCCAAGTAGAG	882
QY	221	LeuValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln	240
DB	883	CTAGTTCACACGGTTCGAACGCATACCCGGAGCTGACGGCAAGTCTTTTCGTTGCGTCAA	942
QY	241	GlnGlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspVal	260
DB	943	CAAGGAGACGATGAGAACCGCAAAATCGAGTGAAGTTGTCACAGGACATAACCGATGTT	1002
QY	261	AlaGlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSer	280
DB	1003	GCTGTCGACACGGTTAAGAAAAACATAGCAACGTTGGGTCGCTGATTTCCCGTTAAGC	1062
QY	281	GluLysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLys	300
DB	1063	GAGAAACTTCTTTTTCGTTACCTTCATGGCAAGAAACTTTTCAAGATAAAATCAAA	1122
QY	301	HisThrThrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGly	320
DB	1123	CATTACTACGTCGCGGTTTCAAACTTGCTATGACCACTTTTGTATACATGCCGGAGGC	1182
QY	321	ArgAlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAla	340
DB	1183	AGAGCCGTGATGATGCTGTAGAGAAACCTAGCCCTAGCACCGCATCGATGTAGAGCA	1242
QY	341	SerArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleThrThrGluLeu	360
DB	1243	TCAAGATCAACGTTACATAGATTTGGAACACTTCATCATGATCAATATGATGATGTTG	1302
QY	361	AlaThrIleGluAlaLysGlyArgMetLysGlyAsnLysValThrGluIleAlaLeu	380
DB	1303	GCATCATAGAACAAAGAGAGGATGAAGAAAGTAAATAGTTGGCAGATGCTTTA	1362
QY	381	GlySerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSer	400
DB	1363	GGGTCAAGCTTTAAGTGTAAACAGTGCAGTTTGGTGGCTCTAAACAATGTCAAAAGCTTCG	1422
QY	401	ThrAsnSerProThrGluHisCysIleAspArgThrProValLysIleAspSerAspSer	420
DB	1423	ACAAATAGTCTCTGGGAACACTGCATCGACAGATACCGGTCAAAATGATTCATTCATCA	1482
QY	421	GlyLysSerGluThrArgValGlnAsnGlyArgSer	432
DB	1483	GGTAAGTCAGAGACTCGTGTCCCAACGCTCGGTCC	1518
RESULT 8			
ID	AAD28504 standard; DNA; 1518 BP.		
XX	AAD28504;		
XX	22-APR-2002 (first entry)		
DE	A. thaliana FAEL-Brassica napus elongase KCS chimeric gene, At74.		
KW	Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;		
KW	very long chain fatty acid; VLCFA; FAEL gene; chimeric; ds.		
XX	Chimeric - Arabidopsis thaliana.		
OS	Chimeric - Brassica napus.		
PH	Key Location/Qualifiers		
FT	CDS 1..1518		
FT	/*tag= a		
FT	/product= "A. thaliana FAEL-Brassica napus elongase KCS		
FT	chimeric protein, At74"		
FT	misc_feature 1..222		
FT	/*tag= b		
FT	/note= "Arabidopsis thaliana FAEL gene"		
FT	223..1518		
FT	misc_feature		
FT	/*tag= c		

FT XX /note= "Brassica napus elongase KCS gene"

PN W0200194565-A2.

XX 13-DEC-2001.

XX 08-JUN-2001; 2001WO-US18737.

XX PF 08-JUN-2000; 2000US-210326P.

XX PR 08-JUN-2000; 2000US-210326P.

XX (UYMI-) UNIV MIAMI.

XX JAWORSKI JG, Blacklock BJ;

XX WPI; 2002-154572/20.

XX P-PSDB; AA017612.

XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic acids encoding the polypeptide, useful for producing very long chain fatty acids

XX Disclosure; Fig 2-5; 139pp; English.

XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase (KCS) polypeptides with altered substrate specificity and/or catalytic activity and nucleic acid molecules encoding such polypeptides.

XX Polypeptides of the invention are useful for catalysing the condensation of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of C20 fatty acyl CoA. They are especially useful for producing very long chain fatty acids (VLCFA) and may be used in the development of reagents for various purposes, e.g., immunological reagents to monitor expression of elongase KCS polypeptides or nucleic acid probes or primers to monitor inheritance of an elongase KCS gene in plant breeding programs. The present sequence is Arabidopsis thaliana FAE1.

XX Brassica napus elongase KCS chimeric gene designated as At74.

SQ Sequence 1518 BP; 415 A; 343 C; 344 G; 416 T; 0 other;

Alignment Scores:

Pred. No.:	1-07e-231	Length:	1518
Score:	2208.50	Matches:	424
Percent Similarity:	99.07%	Conservative:	3
Best Local Similarity:	98.38%	Mismatches:	3
Query Match:	97.94%	Indels:	1
DB:	24	Gaps:	1

SEQ12-JOIN-SEQ4 (1-432) x AAD28504 (1-1518)

QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerVal 21

DB 226 CCGGTTTACCTCGTGTGAGTACTCTGCTACCTCCACCACCGCATGTAGATCAAGTATC 285

QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41

DB 286 TCCAAGGTCATGGATATCTTTATCAAGTAAGAAAGCTGAT--CCTTCGGAACGGC 342

QY 42 ThrCysAspAspSerSerTyrLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61

DB 343 AGTCGGATGACTCCTCGCTGGCTTGACTCTTGAGGAAGATTCAGAACGCTTCAGTCTA 402

QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81

DB 403 GCGCATGAACATCAGCGGCCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTGGC 462

QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101

DB 463 GCGGCGGTGAGAGAGCGGAGCAAGTTATCATTTGCTGAGTAAATCTATTCAAGAAC 522

QY 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121

DB 523 ACCAAGCTTAACCCCTAAGATATAGGTACTTGTGGTGAACCTCAAGCATGTTTATCCA 582

QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141

DB 583 ACTCCATCGCTCCCGCATGGTTCGTTAACACTTTCAAGCTCCGAGCAACGTAAGAAGC 642

QY 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161

DB 643 TTTTACCTTGGTGGCATGGTGTAGTCCGCGCTTATAGCCATTGATCTAGCAAGAGC 702

QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181

DB 703 TTGTTGCATGTCCATAAAATACGTATGCTCTTGTGGTGACACAGAGAACATCATTAT 762

QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201

DB 763 AACATTTACGCTGGTGATAAGTGCATGATGGTTTCAAAATTCGTTGTCGTGTGTGT 822

QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgArgSerLysTyrGluLeu 221

DB 823 GGGGCCGTATTTTGTCTCCCAAGCCCTGGAGATCGTAGCGGCTCAAGTAGCAGCTA 882

QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241

DB 883 GTTCACAGGTTCCGAACGCATACCGGAGCTGACGCAAGTCTTTTCTCGGTGCAACAA 942

QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261

DB 943 GGNAGCATGAGACGCGCAAAATCCGAGTGAGTTGTCCAAGGACATACCGATGTTGCT 1002

QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281

DB 1003 GGTGCAACGGTTAAGAAACATAGCAACGTTGGGTGCGTGTCTTCCGTTAAGCGAG 1062

QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301

DB 1063 AAACITCTTTTTCGTTCCTTCATGGGCAAGAACTTTTCAAAGATAAAATCAAAACAT 1122

QY 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321

DB 1123 TACTACGTCCTCCGGATTCAAACTTGTCTATTGACCATTTTGTATACATGCCGAGGCGAG 1182

QY 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341

DB 1183 GCGGTGATTGATGTCTAGAGAGAACCTAGCCCTAGCACCCTGATGTAGAGGCTCA 1242

QY 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeuAla 361

DB 1243 AGATCAACGTTACATAGATTGGAACACCTTCATCTAGCTCAATATGATGAGTTGGCA 1302

QY 362 TyrIleGluAlaLysGlyArgMetLysGlyAsnLysValTrpGlnIleAlaLeuGly 381

DB 1303 TACATAGAAGCAAAAGGAGGATGAAGAAAGGTAATAAAGTTTGGCAGATTGCTTTAGG 1362

QY 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401

DB 1363 TCAGGCTTTAAGTGTACAGTGCAGTTGGTGGCTCTAAACAATGTCAAAGCTTCGACA 1422

QY 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421

DB 1423 AATAGTCTTGGGAACACTGCTACAGATACCCGCTCAAAATTTGATTTCTGATTAGGT 1482

QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432

DB 1483 ANGTCAGAGACTCGTCTCCAAACGGTCTGCTCC 1515

RESULT 9

AAD28501

ID AAD28501 standard; DNA; 1524 BP.

XX

AC AAD28501;

XX

DT 22-APR-2002 (first entry)

XX

DE Brassica napus fatty acid elongase KCS encoding DNA #1.

XX

KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; ds.
 XX Brassica napus.

OS Key Location/Qualifiers

FT CDS 1..1521

FT /*tag= a

FT /product= "Brassica napus fatty acid elongase KCS

FT protein #1"

XX WO200194565-A2.

XX PD 13-DEC-2001.

XX PF 08-JUN-2001; 2001WO-US18737.

XX PR 08-JUN-2000; 2000US-210326P.

XX PA (UYMI-) UNIV MIAMI.

XX PI Jaworski JG, Blacklock BJ;

XX DR WPI: 2002-154572/20.

XX DR P-PSDB; AAE17609.

XX PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids -
 XX Example 1; Fig 2-2; 139pp; English.

XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
 CC of C20 fatty acyl CoA. They are especially useful for producing very
 CC long chain fatty acids (VLCFA) and may be used in the development of
 CC reagents for various purposes, e.g., immunological reagents to monitor
 CC expression of elongase KCS polypeptides or nucleic acid probes or
 CC primers to monitor inheritance of an elongase KCS gene in plant breeding
 CC programs. The present sequence is Brassica napus fatty acid elongase KCS
 CC encoding DNA.

XX SQ Sequence 1524 BP; 421 A; 350 C; 344 G; 409 T; 0 other;

Alignment Scores:

Pred. No.: 1,07e-231 Length: 1524
 Score: 2208.50 Matches: 424
 Percent Similarity: 99.07% Conservative: 3
 Best Local Similarity: 98.38% Mismatches: 3
 Query Match: 97.94% Indels: 1
 DB: 24 Gaps: 1

SEQ12-JOIN-SEQ4 (1-432) x AAD28501 (1-1524)

Qy 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHiscysArgValSerVal 21
 Db 229 CCGGTTTACCTCGTGTAGTACTCATGCTACCTCCACCACGCATTTGATGCAAGTATC 288
 Qy 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41
 Db 289 TCCAAAGGTCATGGATATCTTTTATCAAGTAAGAAAGCTGAT--CCTTCTCGGAACGGC 345
 Qy 42 ThrCysAspAspSerSerTyrLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
 Db 346 ACGTGGATGATGCTCGTGGCTTACTTCTTGGAGAAATTCAGAGCTTCAGGTCTA 405
 Qy 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
 Db 406 GGCATGAAACATCAGGGCCCGAGGGGCTGCTTACAGTCCCTCCCGGAGACTTTTCG 465

Qy 82 AlaAlaArgGluClnThrGluClnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
 Db 466 GCGGCGGTGAAGAGACGAGCAAGTTATCATTTGGTGGCTAGAAAACTATTCAGAAC 525
 Qy 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
 Db 526 ACCAACGTTAACCTTAAGCATATAGGTATCTTGGTGAACCTCAAGCATGTTTATATCCA 585
 Qy 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
 Db 586 ACTCCATCGCTCTCCGCGATGCTTAAACACTTCAAGCTCCGAAGCAAGTAAGAAGC 645
 Qy 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
 Db 646 TTTAACCTTGGTGGCATGGTGTAGTCCGCGGCTTATAGCCATTGATCAGCAAGAGAC 705
 Qy 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
 Db 706 TTGTTGCATGTCCATAAAAAATACGTATGCTCTTGTGTGAGCAGACAGAAACATCATTAT 765
 Qy 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 Db 766 AACATTTACCTCGTGCATTAATAGTCCCATGATGCTTCAAAATGCTTCTCCGTGTGGT 825
 Qy 202 GlyAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
 Db 826 GGGGCCGCTATTTTGTCTCTCCAAACAGCTGGAGATCGTAGACGGTCCCAAGTAGAGCTA 885
 Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
 Db 886 GTTCACACGGTTCGAACGCATACCGGAGCTGACGGCAAGTCTTTTCTGTTGGTGCACAA 945
 Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
 Db 946 GGAGACGATGAGAACCGCAAAATCGAGTGAAGTTCCTCCAAAGACATAACCGATGTGCT 1005
 Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuProLeuSerGlu 281
 Db 1006 GGTGCAACGGTTAAGAAAACATAGCAACGTGGGTCCGTTGATTTCTCCGTAAAGCGAG 1065
 Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
 Db 1066 AAACCTTTCTTTTCTGTTTACCTTCATGGCAAGAACTTTTCAAGATATAAATCAACAT 1125
 Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyArg 321
 Db 1126 TACTAGTCCCGGATTCAAACTTCCTATTACCATTTTGTATACATCCCGGAGGCAGA 1185
 Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
 Db 1186 GCGGTGATGTATGTGTAGAGAAACCTTAGCCCTAGCAGCATGATGATAGAGGCATCA 1245
 Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleThrPyrGluLeuAla 361
 Db 1246 AGATCAACGTTTACATAGATTGGAAACACTTCACTAGCTCAATATGGTATGAGTTGGCA 1305
 Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
 Db 1306 TACATAGAAGCAAAAGAGGATGAAGAAAGTAAATAAGTTGGCAGATTGCTTAGGG 1365
 Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnAsnValLysAlaSerThr 401
 Db 1366 TCAGGCTTTAAGTGAACAGTGGTCTTGGGTGGCTCTAAACAATGTCAAAGCTTCGACA 1425
 Qy 402 AsnSerProTrpGluHisCysLysAspArgTyrProValLysIleAspSerAspSerGly 421
 Db 1426 AATAGTCTTGGGAACATGTCATCGACAGATACCGGTCAAAATTTGATTCTGATTCAAGT 1485
 Qy 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
 Db 1486 AAGTCAGAACTCTGCTCCAAAACGGTCCGTTCC 1518

RESULT 10

QY 362 TyrIleGluAlaLysGlyArgMetLysGlyAsnLysValTrpClnIleAlaLeuGly 381
 Db 1303 TACATAGAACCAAGGAGGATGAAGAAAGGTAATAAGTTTGGCAGATTGCTTTAGG 1362
 QY 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr 401
 Db 1363 TCAGGCTTTAAGTGTACAGTGCAGTTTGGGTGGCTCTAAACAATGCTCAAAAGCTTCGACA 1422
 QY 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 431
 Db 1423 ANTAGTCTTGGACACATGCAATGACAGATACCGGTCGAATTCATCTGATTCAGGT 1482
 QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
 Db 1483 AAGTCAGAGACTGCTGTGCCAAACACGGTCGGTCC 1515
 RESULT 11
 ID AAD28516 standard; DNA; 1524 BP.
 XX
 AC AAD28516;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Brassica napus fatty acid elongase KCS DNA #1 mutant, Bn G307D.
 KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; mutant; ds.
 XX
 OS Brassica napus.
 XX
 FH Key Location/Qualifiers
 CDS 1..1521
 FT /tag= a
 FT /product= "Brassica napus fatty acid elongase KCS
 FT protein #1 mutant Bn G307D"
 FT mutation replace (920, G)
 FT /*tag= b
 XX
 PN WO200194565-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 08-JUN-2001; 2001WO-US18737.
 XX
 PR 08-JUN-2000; 2000US-210326P.
 XX
 PA (UIMI-) UNIV MIMI.
 XX
 PI Jaworski JG, Blacklock BJ;
 XX
 DR WPI; 2002-154572/20.
 DR P-PSDB; AAE17624.
 XX
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 XX
 PS Disclosure; Fig 2-17; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
 CC of C20 fatty acyl CoA. They are especially useful for producing very
 CC long chain fatty acids (VLCFA) and may be used in the development of
 CC reagents for various purposes, e.g., immunological reagents to monitor
 CC expression of elongase KCS polypeptides or nucleic acid probes or
 CC primers to monitor inheritance of an elongase KCS gene in plant breeding
 CC programs. The present sequence is a mutant of Brassica napus fatty acid
 CC elongase KCS protein #1 encoding DNA designated as Bn G307D.

XX SQ Sequence 1524 BP; 422 A; 350 C; 343 G; 409 T; 0 other;
 Alignment Scores:
 Pred. No.: 6, 28e-231 Length: 1524
 Score: 2201.50 Matches: 423
 Percent Similarity: 98.84% Conservative: 3
 Best Local Similarity: 98.14% Mismatches: 4
 Query Match: 97.63% Indels: 1
 DB: 24 Gaps: 1
 SEQ12-JOIN-SEQ4 (1-432) x AAD28516 (1-1524)
 QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerVal 21
 Db 229 CCGGTTTACCTCGTGTGAGTACTCATGCTACCTCCACCAACGATTTAGATCAAGTATC 288
 QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
 Db 289 TCCAAGGTCATGCATATCTTTTATCAAGTAGAAGAGCTGAT---CCTTCTCGGACGGC 345
 QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
 Db 346 ACGTGCATGACTCGTGGTGGCTTACTTCTGTAGGAAGATTCAAGAACGTCAGGTCTA 405
 QY 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
 Db 406 GCGCATGAAACTCACGGGCCCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTGG 465
 QY 82 AlaAlaArgGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
 Db 466 GCGGCGCTGAAGACGAGGAGCAAGTTATCATTTGGTGGCTAGAAAATCTATTCAAGAAC 525
 QY 102 ThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnPro 121
 Db 526 ACCACAGTTAACCTTAAGATATAGGTATAGTGTGGTGAACCTCAAGCATGTTTAATCCA 585
 QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
 Db 586 ACTCATCGCTCTCCGCGATGCTGTTTAAACACTTTCAGCTCCGAAGCAAGCTAAGAAC 645
 QY 142 PheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
 Db 646 TTTAACCTTGGTGGCATGGTTGTAGTCCCGCGCTTATAGCCATTGATCAGCAAGGAC 705
 QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
 Db 706 TTGTTGATGTTCATATAAAATACGTATGCTCTTGTGTGAGCAGACAGAACATCACTTAT 765
 QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 Db 766 AACATTTACGCTGTGTATATAGTCCCATGATGTTTCAAAATGCTTGTTCGTTGGT 825
 QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgArgSerLysTyrGluLeu 221
 Db 826 GGGGCGCTATTGTTCTCTCCAAACANGCTCGAGTCTGAGTCCCAAGTACAGCTA 885
 QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
 Db 886 GTTCACACGGTTCGAACGATACCGGAGCTCAGCACAAGTCTTTTTCGTTGGTGCACAA 945
 QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
 Db 946 GGAGACGATGAGAACGGCAAAATCGAGTGTGTTGCCAAGCACAATAACCGATGTTGCT 1005
 QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
 Db 1006 GGTGACAGGTTAGAAAACATACACACGTTGGTCCGTTGATCTTCCTGTTAAGCGAG 1065
 QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
 Db 1066 AAACCTTCTTTTTCGTTACCTTCATGGCAAGAAACCTTTTCAAGATAAAATCAACAT 1125

Db 891 GGTGCAAGCGTTAAGAAACATACCAACGTTGGTCCGTTGATTCCTCCGTTAAGCGAG 950
 QY 282 LysLeuLeuPheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis 301
 Db 951 AAACCTCTTTTTCGTTTACCTTCATGGGCAAGAACTTTCAAGATANAATCAACAT 1010
 QY 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyIleYarg 321
 Db 1011 TACTACGTCGGGATTCAACTTCTATTGACCATTTTGTATATACATGCCGGAGGCAGA 1070
 QY 322 AlaValIleAspValLeuGlyLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
 Db 1071 GCCGTGATGATGTGTAGAGAAACCTAGCCCTAGCACCATCGATGTAGAGGCATCA 1130
 QY 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeuAla 361
 Db 1131 AGATCAACGTTACATAGATTTGGAAACACTTCATCTAGCTCAATATGTTAGTTGGCA 1190
 QY 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
 Db 1191 TACATAGAACAAAGGAAGGATGAAGAAAGGTAATAAAGTTTGGCAGATTGCTTAGGG 1250
 QY 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr 401
 Db 1251 TCAGGCTTTAAGTGAACAGTCAGTTCAGTTGGGTGGCTCTAACAATGTCAAGCTTTCACA 1310
 QY 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
 Db 1311 AATAGTCCTTTGGGAACACATGCATCGACAGATACCCTGTCATAATGATCTGATTCAGGT 1370
 QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
 Db 1371 AAGTCAGAGACTCGTGTCAAAAACGTCGGTCC 1403
 RESULT 13
 ID AAF61744 standard; cDNA; 1785 BP.
 XX AC AAF61744;
 XX DT 12-JUL-2001 (first entry)
 XX DE B. napus KCS cDNA SEQ ID 1.
 KW KCS; beta-ketoacyl-CoA-synthase; transgenic plant; long-chain fatty acid;
 KW cleaning composition; cosmetic; dye additive; lubricant; preservative;
 KW plasticizer; seed-specific expression; fatty acid biosynthesis;
 KW lipid metabolism; ss.
 XX OS Brassica napus.
 XX PN WO200129238-A2.
 XX PD 26-APR-2001.
 XX PF 20-OCT-2000; 2000WO-BP10363.
 XX PR 20-OCT-1999; 99DE-1050589.
 XX PA (ERWE-) GES ERWERB & VERW VON SCHUTZRECHTEN-GVS.
 XX PI Wolter FP, Han J, Frentzen M;
 XX DR WPI; 2001-273877/28.
 XX PT New nucleic acid encoding beta-ketoacyl-CoA-synthase from Brassica
 XX napus, useful for preparing transgenic plants with high content of very
 XX long, optionally unsaturated, fatty acids
 XX PS Claim 2; Page 54-55; 59pp; German.
 XX CC This invention describes a novel nucleic acid (I) encoding a protein
 CC (II), from Brassica napus, with beta-ketoacyl-CoA-synthase (KCS)

CC activity. (I) is used to generate transgenic plants or microorganisms
 CC with increased content of long-chain fatty acids, especially increased
 CC ratio of 22:1 to 20:1, relative to the wild type. These fatty acids are
 CC variously useful as (or for producing) e.g. cleaning compositions,
 CC cosmetics, dye additives, lubricants, preservatives, plasticizers etc.
 CC Where the fatty acids are polyunsaturated, they are also useful in
 CC nutrition and pharmaceuticals. A promoter (Ia), from (I), is used to
 CC provide seed-specific expression of other genes linked to it,
 CC particularly those involved in fatty acid biosynthesis or lipid
 CC metabolism, but also for 'switching off' selected genes by antisense or
 CC co-suppression methods. (I), encoding an enzyme that catalyzes elongation
 CC of fatty acid chains, increases the proportion of the more valuable
 CC longer chain fatty acids at the expense of shorter chain acids. A vector
 CC containing the napin promoter; the KCS sequence of B. napus and the polyA
 CC signal from the same gene, was used to transform the low-erucic acid rape
 CC variety Drakkar. The fatty acid distribution of one selected T2 line was
 CC 7.3% 20:1; 5.6% 22:1 and 0.4% 24:1, i.e. 13.3 wt.% total very long chain
 CC fatty acids. Comparable figures for the parent variety were 1.9%; 0.1%
 CC and 0.3% (2.3% total). This sequence encodes a Brassica napus KCS protein
 CC described in the method of the invention.

XX SQ Sequence 1785 BP; 507 A; 394 C; 381 G; 503 T; 0 other;

Alignment Scores:
 Pred. No.: 7,93e-231 Length: 1785
 Score: 2201.50 Matches: 423
 Percent Similarity: 98.84% Conservative: 3
 Best Local Similarity: 98.14% Mismatches: 4
 Query Match: 97.63% Indels: 1
 DB: 22 Gaps: 1

SEQ12-JOIN-SEQ4 (1-432) x AAF61744 (1-1785)

QY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerVal 21
 Db 310 CCGGTTTACCTCGTTGAGTACTCATCTTCCACCAACGATTTAGTCAAGTATC 369
 QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerArgAsnGly 41
 Db 370 TCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAGCTGAT---CCTTCTCGGAACGGC 426
 QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
 Db 427 ACGTGGCATGACATCGCTGCGGCTTGACTCTTGGGAAGATTCAGAAGCTGCTA 486
 QY 62 GlyAspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAla 81
 Db 487 GCGCATGAAGAACTCACGGGCCCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTGGC 546
 QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
 Db 547 GCGGCGGTGAAGAGACGGAGCAAGTTATCATTTGGTGGCTAGAAAAATCTATTCAAGAAC 606
 QY 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
 Db 607 ACCAACGTTAACCTTAACATATAGTATAGTATCTGTGGTGAACCTCAAGCATGTTTATCCA 666
 QY 122 ThrProSerLeuSerAlaMetValValIleAsnThrPheLysLeuArgSerAsnValArgSer 141
 Db 667 ACTCCATCGCTCTCCCGCATGGTGTGTAACACATTTCAAGCTCCGGAAGCAAGCTAAGAAC 726
 QY 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
 Db 727 TTTAACCTTGGTGGCATGGTTGTAGTCCGGGGCTTATAGCCATTGATCAGCAAGGAC 786
 QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
 Db 787 TGTGTGATGTCTCCATAAATAACGTATGCTCTGTGTGAGCACAGAACATCATTAT 846
 QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 Db 847 AACATTTACGCTGTGATATAATAGTCCATGATGTTTCAAAATTTGCTTGTCCGTGTTGGT 906

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Qy 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
Db 907 GGGGCGCTATTTGCTCTCCAAAGAGCTGGAGATCGTAGCGGTCCAAAGTACGAGCTA 966
Qy 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
Db 967 GTTCACGGGTTCGAACGCATACCGGAGCTGACGACAAAGTCTTTTGGTGGCGCAACA 1026
Qy 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
Db 1027 GGAGACGTGAGACGCCAANAATCGGAGTGAGTTGTCCAAAGACATACCATGTTGCT 1086
Qy 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuLeuLeuProLeuSerGlu 281
Db 1087 GGTCCGAACGGTTAGAAAACATAGCAAGTTGGTGGCTGGTGAATCTTCGTAAAGCGAG 1146
Qy 282 LysLeuLeuPhePheValThrPheMetGlyLysLysLysLeuPheLysAspLysIleLysHis 301
Db 1147 AAACCTCTTTTTCGTTTACCTTTCATGGGCAAGAACTTTTCAAAGATAAAATCAACAT 1206
Qy 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
Db 1207 TACTAGCTCCGGATTTCAAACTTGCTATTGACCATTTTGTATACATGCCGGAGCGAGA 1266
Qy 322 AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
Db 1267 GCGGTGATGATGCTAGAGAAGAACCTAGCCCTAGCAGCGATCGATGAGGACATCA 1326
Qy 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTrpTyrGluLeuAla 361
Db 1327 AGATCAAGCTTACATAGATTGTGAAACACTTTCATAGCTCAATATGCTATGAGTTGCA 1386
Qy 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTrpGlnIleAlaLeuGly 381
Db 1387 TACATAGAAGCAAAAGAGGATGAAGAAAGTAAATGAAGTTGGCAGATTCTTTAGG 1446
Qy 382 SerGlyPheLysCysAsnSerAlaValTrpValAlaLeuAsnValLysAlaSerThr 401
Db 1447 TCAGGCTTTAGTGTACAGTCGCTGTTGGTGGCTCTAAACATGTCAAACTTCGAC 1506
Qy 402 AsnSerProTrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
Db 1507 AATAGTCCTTGGGAACACTGCATCGACAGATACCGGCTCAAAATTTGATTCTGATTCAGT 1566
Qy 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
Db 1567 AAGTCAGAGACTCGTGTCCAAACGGTCGGTCC 1599
RESULT 14
AAF61746
XX AC AAF61746
XX DT 12-JUL-2001 (first entry)
XX DE B. napus KCS cDNA SEQ ID 3.
XX KW KCS: beta-ketoacyl-CoA-synthase; transgenic plant; long-chain fatty acid;
XX KW cleaning composition; cosmetic; dye additive; lubricant; preservative;
XX KW plasticizer; seed-specific expression; fatty acid biosynthesis;
XX KW lipid metabolism; ss.
XX OS Brassica napus.
XX FH Key Location/Qualifiers
XX CD 82..1602
XX FT /*tag= a "KCS"
XX ET /product= "KCS"
XX WC200129238-A2.
XX FN
XX XX 26-APR-2001.
XX PD
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XX 20-OCT-2000; 2000WO-EPI0363.
XX 20-OCT-1999; 99DE-1050589.
XX (ERWE-) GES ERWERB & VERW VON SCHUTZRECHTEN-GVS.
XX Wolter FP, Han J, Frentzen M;
XX WPI: 2001-273877/28.
XX P-PSDB; AAB70888.
XX New nucleic acid encoding beta-ketoacyl-CoA-synthase from Brassica
XX napus, useful for preparing transgenic plants with high content of very
XX long, optionally unsaturated, fatty acids -
XX Claim 2: Fig 1; 59pp; German.
XX This invention describes a novel nucleic acid (I) encoding a protein
XX (II), from Brassica napus, with beta-ketoacyl-CoA-synthase (KCS)
XX activity. (I) is used to generate transgenic plants or microorganisms
XX with increased content of long-chain fatty acids, especially increased
XX ratio of 22:1 to 20:1, relative to the wild type. These fatty acids are
XX variously useful as (or for producing) e.g. cleaning compositions,
XX cosmetics, dye additives, lubricants, preservatives, plasticizers etc.
XX Where the fatty acids are polyunsaturated, they are also useful in
XX nutrition and pharmaceuticals. A promoter (Ia), from (I), is used to
XX provide seed-specific expression of other genes linked to it,
XX particularly those involved in fatty acid biosynthesis or lipid
XX metabolism, but also for 'switching off' selected genes by antisense or
XX co-suppression methods. (I), encoding an enzyme that catalyzes elongation
XX of fatty acid chains, increases the proportion of the more valuable
XX longer chain fatty acids at the expense of shorter chain acids. A vector
XX containing the napin promoter; the KCS sequence of B. napus and the polyA
XX signal from the same gene, was used to transform the low-erucic acid rape
XX variety Drakkar. The fatty acid distribution of one selected T2 line was
XX 7.3% 20:1, 5.6% 22:1 and 0.4% 24:1, i.e. 13.3 wt.% total very long chain
XX fatty acids. Comparable figures for the parent variety were 1.9%; 0.1%
XX and 0.3% (2.3% total). This sequence encodes a Brassica napus KCS protein
XX described in the method of the invention.
XX SQ Sequence 1785 BP; 507 A; 394 C; 381 G; 503 T; 0 other;
Alignment Scores:
Pred. No.: 7,93e-231 Length: 1785
Score: 2201.50 Matches: 423
Percent Similarity: 98.84% Conservative: 3
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 97.63% Indels: 1
DB: 22 Gaps: 1
SEQ12-JOIN-SEQ4 (1-432) x AAF61746 (1-1785)
Qy 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProHisCysArgValSerVal 21
Db 310 CCGGTTTACCTCGTTGAGTACTACTGCTACCTCCACCACGCATTTGATCAAGTATC 369
Qy 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAnGly 41
Db 370 TCCAGGTCATGGATATCTTTTATCAAGTAGAAGAAAGCTGAT---CCTTCTCGGAACGGC 426
Qy 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
Db 427 AGTGCATGACTCGTGGCTTGACTTCTTGAGGAAGATTCAAGAAGCTTCAGGTCTA 486
Qy 62 GlyAspGluThrHisGlyProGluGlyLeuLeuGlnValProProArgLysThrPheAla 81
Db 487 GCGGATGAACATCAGGCGCCGAGGGGCTGCTTCAGTCCCTCCCGGAAGACTTTTCGG 546
Qy 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
Db 547 GCGGCGCTGAAGACGAGCAAGTATTCATTTGTCGCTAGAAAATCTATTATTCAGAAC 606
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QY 102 ThrAsnValAsnProLysAspIleGlyLeuValValAsnSerSerMetPheAsnPro 121
DB 607 ACCAAGCTTAACCTTAAGATATAGGTATACCTGGTGAACCTCAAGCATGTTTAATCCA 566
QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
DB 667 ACTCATCGCTCGCGCATGGTGGTAAACACTTCAAGCTCCGAAGCAACGTAAGAAGC 726
QY 142 PheAsnLeuGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
DB 727 TTTAACTTGGTGGCATGGTGTAGTCCCGCTTATAGCCATTGATAGCAAGGAC 786
QY 162 LeuLeuHisValHisLysAsnThrTyrAlaLeuValValSerThrGluAsnIleThrTyr 181
DB 787 TTGTTGCATGCTCAAAAATACGTATGCTTGTGGTGAGCAGACAGACATCATTTAT 846
QY 182 AsnIleTyrAlaGlyAspAsnArgSerMetValSerAsnCysLeuPheArgValGly 201
DB 847 AACATTTACGCTGGTGAATAGTCCATGATGGTTTCAAAATGCTTGTTCGCTGGT 906
QY 202 GlyAlaAlaIleLeuSerAsnLysProGlyAspArgArgSerLysTyrGluLeu 221
DB 907 GGGGCGCTATTTGCTCTCCAACAAGCCTGGAGATCGTAGAGCTCCAAGTACGAGCTA 966
QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGln 241
DB 967 GTTCACACGGTTCGAACGCATACCGGAGCTGACGACAAGCTCTTTCGTTGGTGCACAA 1026
QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
DB 1027 GGAGACGATGAGAAGCGCAAAATCGGAGTGTGTTGTCACAGGACATAACCGATGTTGCT 1086
QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
DB 1087 GCTCGAAGGTTAAGAAAACAATAGCAACGCTGGGTCCTGTATCTTCCTTAAGCGAG 1146
QY 282 LysLeuLeuPhePheValThrPheMetGlyLysLeuPheLysAspLysIleLysHis 301
DB 1147 AAATCTCTTTTTCGTTACCTTCATCGGCAAGAAACTTTTCAAGATPAAATCAACAT 1206
QY 302 TyrTyrValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg 321
DB 1207 TACTACGCTCCGGATTCAAACTTGCTATTGACCAATTTTGTATACATGCGGAGGCGA 1266
QY 322 AlaValIleAspValLeuCluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer 341
DB 1267 GCCGTGATTGATGCTAGAGAAGAACTAGCCCTAGCACCCATCGATGATAGAGGCATCA 1326
QY 342 ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerIleTyrTyrGluLeuAla 361
DB 1327 AGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGTTAGTTGGCA 1386
QY 362 TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTyrGlnIleAlaLeuGly 381
DB 1387 TACATAGACCAAAAGAGGATGAGNAAGGTAAATAAGTTGGCAGATTGCTTAGGG 1446
QY 382 SerGlyPheLysCysAsnSerAlaValTyrPvalAlaLeuAsnValLysAlaSerThr 401
DB 1447 TCAGGCTTTAAGTGTAAACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAAGCTTCGACA 1506
QY 402 AsnSerProtrpGluHisCysIleAspArgTyrProValLysIleAspSerAspSerGly 421
DB 1507 AATAGTCCTTGGGAACACTGCATCGACAGATACCGCGTCAAAATGATTCTGATTACGTT 1566
QY 422 LysSerGluThrArgValGlnAsnGlyArgSer 432
DB 1567 AAGTCAGAGACTCGTGTCCAAACAGGTCGGTCC 1599
RESULT 15
AAF62741
ID AAF62741 standard; DNA; 1790 BP.
XX
AC AAF62741;
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XX 02-MAY-2001 (first entry)
DE Brassica napus FAEL promoter.
XX Brassica napus; FAEL; fatty acid elongation 1;
KW seed-specific gene expression; transgenic plant; seed development;
KW seed lipid metabolism; ds.
XX Brassica napus.
XX WO200111061-A2.
PD 15-FEB-2001.
XX 04-AUG-2000; 2000WO-CA00907.
XX 04-AUG-1999; 99US-0147133.
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX Kunst L, Clemens S;
XX WPI; 2001-191548/19.
XX Recombinant nucleic acid for mediating seed-specific expression in
PT Arabidopsis, comprises a heterologous promoter with a transcriptional
PT regulatory region of the 5' region of a plant fatty acid elongation 1
PT gene
XX Disclosure; Fig 2; 41pp; English.
XX The present sequence is the promoter of the Brassica napus FAEL
CC (fatty acid elongation 1) gene. Nucleic acid constructs comprising
CC transcriptional regulatory regions homologous to plant FAEL promoters may
CC be used in transgenic cells or plants to promoter expression of foreign
CC and endogenous genes in developing seeds. The constructs are used to
CC promote expression of foreign and endogenous genes in developing seeds,
CC to affect seed lipid metabolism, protein or carbohydrate composition and
CC accumulation, or seed development. Transcriptional regulatory regions of
CC the FAEL gene may be useful for the production of modified seeds
CC containing novel recombinant proteins which have pharmaceutical,
CC industrial or nutritional value. The nucleic acids may also be used as
CC plant breeding tools, as molecular markers to aid in plant breeding
CC programmes. Such techniques include using the gene as a molecular probe
CC or using the DNA sequence to design PCR primers for use in screening
CC techniques.
XX Sequence 1790 BP; 494 A; 401 C; 384 G; 511 T; 0 other;
```

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Alignment Scores:
Pred. No.: 7,97e-231 Length: 1790
Score: 2201.50 Matches: 423
Percent Similarity: 98.84% Conservative: 3
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 97.63% Indels: 1
DB: 22 Gaps: 1
SEQ12-JOIN-SEQ4 (1-432) x AAF62741 (1-1790)
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```
QY 2 ProValTyrLeuValAspTyrSerCystTyrLeuProProHisCysArgValSerVal 21
DB 136 CCGGTTTACCTCGTGGTACTCATGCTACTCTCCACCAACGATGTAGATCAAGTATC 185
QY 22 SerLysValMetAspIlePheTyrGlnIleArgLysAlaAspThrSerSerArgAsnGly 41
DB 186 TCCAAAGGTCAATGATATCTTTATCAAGTAAGAAGAGCTGAT---CCTTCTCGGAAGCGC 242
QY 42 ThrCysAspAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
DB 243 ACGTGCATGACCTCGTGGCTGCTGACTTCTTGAGGAAGATTCAAGAACGTTACAGTCTA 302
QY 62 GlyAspGluThrHisGlyProGluGlyLeuGlnValProProArgLysThrPheAla 81
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Db 1383 AAGTCAGAGACTCGTGTCCAAAACGGTCGGTCC 1415

Search completed: January 6, 2003, 16:49:07
Job time : 213 secs

303	Db		GGCGATGAACCTCACGGGGCCGAGGGGGTCTTCAGGTGCTCCCGGAAGACTTTTGGC	362
82	Qy		AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn	101
363	Db		CGGGCGGTGAAGACGCGGCAAGTTATCATTTGGTGGCTAGATAAATCTATTCAAGAAC	422
102	Qy		ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro	121
423	Db		ACCAACGTTAAACCCCTAAAGATATAGGTATCTTGGTGGAATCAAGCATGTTTAAATCCA	482
122	Qy		ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer	141
483	Db		ACTCCATCGCTCTCCGGATGGTGTAAACACTTTCAAGCTCCGAAGCAACGTAAAGAAGC	542
142	Qy		PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp	161
543	Db		TTTAAACCTTTGGTGGCATGGGTGTAGTGGCGGGCTTATGCCATGTATCAGCAAGAGAC	602
162	Qy		LeuLeuHisValHisLysAsnThrTyAlaLeuValValSerThrGluAsnIleThrTy	181
603	Db		TTGTTCGATGTCCATAAAATACGTATGCTCTTGTGGTGAGCACAGAAACATCACATTAT	662
182	Qy		AsnIleTyAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly	201
663	Db		AACATTTAGCGTGGTGATATAGTCCATGATGGTTTCAATTCCTTGTTCGGTGTGGT	722
202	Qy		GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyThrGluLeu	221
723	Db		GGGGCGGTATTTTGTCTCTCAACAAAGCCGTGAGATCGTAGAGGGTCCAAAGTACGAGCTA	782
222	Qy		ValHisThrValAcqThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln	241
783	Db		GTTACACAGGTTTCGAACGCATACCGAGCTGACAGCAAGTCTTTTTCGTGGCTGCACAA	842
242	Qy		GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla	261
843	Db		GGAGAGATGAGAACGGCAAAATCGAGTGAGTTTGTCCAAAGGACATAACCGATGTGGCT	902
262	Qy		GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu	281
903	Db		GGTGCAAACGGTTAAGAAACATAGCAACGTTGGGTCCGTGATTCTTCCGTTAAGCGAG	962
282	Qy		LysLeuLeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHis	301
963	Db		AAACTCTTTTTCGTTTACCTTCATGGGCAAGAACTTTTCAAAGATAAAAATCAACAT	1022
302	Qy		TyTyTyValProAspPheLysLeuAlaIleAspHisPheCysIleHisAlaGlyGlyArg	321
1023	Db		TACTACGTCCCGGATTTCAACTTGTCTNTTGACATTTTGTATACATGCCGAGGCGAGA	1082
322	Qy		AlaValIleAspValLeuGluLysAsnLeuAlaLeuAlaProIleAspValGluAlaSer	341
1083	Db		CGCGTGATTGATGTCTAGAGAAGAACCTAGCCCTAGCACCGATGATGTAGAGCATCA	1142
342	Qy		ArgSerThrLeuHisArgPheGlyAsnThrSerSerSerSerIleTyTyTyGluLeuAla	361
1143	Db		AGATCAACGTTACATAGATTTTGGAACACTTCATCTACATATGGTATCAGTTGGCA	1202
362	Qy		TyrIleGluAlaLysGlyArgMetLysLysGlyAsnLysValTyProGlnIleAlaLeuGly	381
1203	Db		TACATAGAGCAAAAGGAAGGATGGAAGAAGTATAAAGTTTGGCAGATTGTCTTTAGGG	1262
382	Qy		SerGlyPheLysCysAsnSerAlaValTyProValAlaLeuAsnAsnValLysAlaSerThr	401
1263	Db		TCAGGCTTTAAGTGTAAACGTGACGTTGGTGGCTCTAAACAATGTCAAAGCTTCGACA	1322
402	Qy		AsnSerProTyProGluHisCysIleAspArgTyTyProValLysIleAspSerAspSerGly	421
1323	Db		AATAGTCTTGGGAACACTGCATCGACAGATACCGCGTCAAAATTTGATTCTGATTCAGGT	1382
422	Qy		LysSerGluThrArgValGlnAsnGlyArgSer	432

Db 289 TCCAGGTCATGGATATCTTTTCAAGTAAGAAAGCTGAT---CCCTTCGGAAGCGC 345
 QY 42 ThrCysAspSerSerTrpLeuAspPheLeuArgLysIleGlnGluArgSerGlyLeu 61
 Db 346 ACCTGCGATGACCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 405
 QY 62 GlyAspGluThrHisGlyProGluGluLeuGlnValProProArgLysThrPheAla 81
 Db 406 GCGGATGAACATCAAGGCGCCGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465
 QY 82 AlaAlaArgGluGluThrGluGlnValIleIleGlyAlaLeuGluAsnLeuPheLysAsn 101
 Db 466 GCGGCGCTGAAGACGAGCAAGTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525
 QY 102 ThrAsnValAsnProLysAspIleGlyIleLeuValValAsnSerSerMetPheAsnPro 121
 Db 526 ACCACGTTTAACTTAAGTATAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
 QY 122 ThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArgSer 141
 Db 586 ACTCATCGCTCTCCGCGATGCTGCTTAAACACTTCAAGCTCGAAGCAACGTAAGAACG 645
 QY 142 PheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleAlaIleAspLeuAlaLysAsp 161
 Db 646 TTTAACCTTGTGTCATGGTGTAGTCCGCGCTTATAGCCATTGATCTAGCAAGGAC 705
 QY 162 LeuLeuHisValHisLysAsnThrThrAlaLeuValValSerThrGluAsnIleThrTyr 181
 Db 706 TTGTTGATGCTTCAAAAATAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765
 QY 182 AsnIleThrAlaGlyAspAsnArgSerMetMetValSerAsnCysLeuPheArgValGly 201
 Db 766 AACATTACGCTGTGATAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 825
 QY 202 GlyAlaAlaIleLeuLeuSerAsnLysProGlyAspArgArgSerLysTyrTrpGluLeu 221
 Db 826 GGGCGCTATTTGCTCTCAACAGCTGGAGATCGTAGCGTCAAGTACGAGCTA 885
 QY 222 ValHisThrValArgThrHisThrGlyAlaAspGlyLysSerPheArgCysValGlnGln 241
 Db 886 GTTACACGGTTTCAAGCATACCGGAGCTGACGCAAGTCTTTTCTGCTGCTGCAACAA 945
 QY 242 GlyAspAspGluAsnGlyLysIleGlyValSerLeuSerLysAspIleThrAspValAla 261
 Db 946 GGAGACGATGAGACGCAAAATCGAGTGTGTTGCTCAAGGACATACCGATGCTGCT 1005
 QY 262 GlyArgThrValLysLysAsnIleAlaThrLeuGlyProLeuIleLeuProLeuSerGlu 281
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 ACCESSION AF009563
 VERSION AF009563.1 GI:2271464
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 SOURCE Brassica napus.
 ORGANISM Brassica napus
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE
 AUTHORS Clemens, S. and Kunst, L.
 TITLE Isolation of a Brassica napus cDNA (Accession No. AF009563) encoding 3-ketoacyl-CoA synthase, a condensing enzyme involved in the biosynthesis of very long chain fatty acids in seeds (PCR97-125)
 JOURNAL Plant Physiol. 115, 313-314 (1997)
 REFERENCE
 AUTHORS Clemens, S. and Kunst, L.
 TITLE Direct Submission
 JOURNAL Submitted (19-JUN-1997) Botany, University of British Columbia, 6270 University Blvd., Vancouver, BC V6T 1Z4, Canada
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DEFINITION AX358173
ACCESSION AX358173
VERSION AX358173.1 GI:18674882
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaworski, J.G. and Blacklock, B.J.
TITLE Fatty acid elongase 3-ketoacyl coA synthase polypeptides
JOURNAL Patent: WO 0194565-A 17 13-DEC-2001;
MIAMI UNIVERSITY (US)
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SEQ12-JOIN-SEQ4 (1-432) x AX358173 (1-1518)
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